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Publication number: **0 416 725 A2**

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EUROPEAN PATENT APPLICATION

⑪ Application number: 90307566.1

⑪ Int. Cl.⁸: **C12N 15/51, C07K 15/00,
//A61K39/29, G01N33/576**

⑫ Date of filing: 11.07.90

The microorganisms have been deposited with
Fermentation Research Institut, Japan under
numbers: FERM BP 2951 - 2968.

The title of the invention has been amended
(Guidelines for Examination in the EPO, A-III,
7.3).

⑬ Priority: 14.07.89 JP 182073/89
19.07.89 JP 184739/89
22.07.89 JP 189874/89
27.07.89 JP 192721/89
29.07.89 JP 195413/89
03.08.89 JP 200217/89
10.08.89 JP 205722/89
21.09.89 JP 243304/89
22.09.89 JP 245268/89
19.10.89 JP 270398/89

⑭ Date of publication of application:
13.03.91 Bulletin 91/11

⑮ Designated Contracting States:
AT BE CH DE DK ES FR GB GR IT LI NL SE

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⑳ Blood-borne non-A, non-B hepatitis specific protein, DNA encoding it, and process for its production.

㉑ A DNA coding for a blood-borne non-A, non-B hepatitis specific antigenic protein and corresponding to an RNA directly isolated from a human blood or liver tissue is disclosed. This antigenic protein can be produced by using the DNA, and the antigenic protein binds to an antibody in the serum of the patient with the non-A, non-B hepatitis. Therefore, the antigenic protein is useful for the diagnostic measurement of an antibody against the non-A, non-B hepatitis specific antigen.

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BLOOD-BORNE NON-A, NON-B HEPATITIS SPECIFIC ANTIGENIC PROTEIN, A DNA CODING FOR THE PROTEIN AND A PROCESS FOR PRODUCING THE PROTEIN

TECHNICAL FIELD

The present invention relates to a novel protein and a DNA fragment. More particularly, it relates to a blood-borne non-A, non-B hepatitis specific antigenic protein which appears specifically on the pathogenesis of blood-borne non-A, non-B hepatitis, a DNA fragment coding for the protein, and a process for producing the protein by using the DNA fragment.

BACKGROUND ART

The viruses of the viral hepatitis type A and type B have been discovered, the hepatitis has been successfully diagnosed by the immunological method, and vaccines for these viruses have been developed. Nevertheless, currently the entity of the hepatitis which is neither type A nor type B, i.e., non-A, non-B hepatitis, is not clear, since the pathogenic virus is present only in an extremely small quantity in organisms. Blood-borne non-A, non-B hepatitis is responsible for 90% of the occurrences of post-transfusion hepatitis, which occurs in 10 to 20% of transfused patients [Experimental Medicine vol. 7, 196 - 201 (1988)].

Research into antigenic protein associated with blood-borne non-A, non-B hepatitis has been made by various researchers using patient's blood as samples. For example, Choo et al. described in Science, 244, 359 - 362 (1989) and European Unexamined Patent Publication No. 0318 216 A1, that a chimpanzee was infected with hepatitis by infusing the blood of a patient suffering from blood-borne non-A, non-B hepatitis, RNA was then extracted from the serum of the chimpanzee, and a fragment of a non-A, non-B hepatitis virus gene was isolated from a cDNA library prepared from the RNA. Further, it has been reported that blood infected with non-A, non-B hepatitis can be diagnosed at a probability of 60 - 70% of the blood samples infected with non-A, non-B hepatitis virus, as a result of the blood sample test carried out in Japan using an immunological diagnostic reagent based on the afore-mentioned virus gene fragment (KOSEISHO KAN-EN KENKYU RENRAKU KYOGIKAI HOKOKU 1989, 3, 13).

On the other hand, Japanese Unexamined Patent Publication No. 2576/1989 disclosed that a chimpanzee was infected with non-A, non-B hepatitis by infusing the blood of a patient suffering from the hepatitis, RNA was extracted from the liver cell of the chimpanzee, and using the extracted RNA, the gene coding the non-A, non-B hepatitis specific antigenic protein was cloned.

The former report gives insufficient information, in that the diagnostic reagent has a low diagnostic probability for blood infected with the non-A, non-B hepatitis virus, the cloned gene as described in that paper has an insufficient number of bases, compared with the assumed number of bases of the blood-borne non-A, non-B hepatitis virus gene, and there is a possibility that two or more kinds of the blood-borne non-A, non-B hepatitis viruses exist.

In the latter report, no direct evidence is shown that the cloned gene is specific to human non-A, non-B hepatitis.

In both of the investigations described above, RNA obtained through a chimpanzee was used and not RNA extracted directly from human patients suffering from the blood-borne non-A, non-B hepatitis, and thus it remains uncertain whether or not the cloned DNA truly reflects the gene for the human non-A, non-B hepatitis virus. Accordingly, new approaches must be made to meet the demand for the development of a diagnostic reagent having a higher diagnostic probability, and a vaccine.

As one such approach, one of the present inventors extracted RNA directly from the blood of human patients with non-A, non-B hepatitis, and reported successful results with a method to be described hereinafter [Experimental Medicine, Vol. 7, 196 - 201 (1989)].

DISCLOSURE OF THE INVENTION

The present inventors conducted intensive research into the solving of the aforementioned problems, and as a result, succeeded in directly extracting RNA from the liver cell or blood of human patients with non-A, non-B hepatitis, and from this RNA cloning DNAs coding for a blood-borne non-A, non-B hepatitis specific antigenic proteins.

Therefore, the present invention provides DNAs coding for a blood-borne non-A, non-B hepatitis specific antigenic protein which appears in a human liver cell and/or blood upon the pathopoiesis of a blood-borne non-A, non-B hepatitis.

The present invention also provides a process for preparing the blood-borne non-A, non-B hepatitis specific antigenic protein, comprising culturing a host transformed by an expression vector containing the DNA.

The present invention further provides the proteins produced by the above-described process.

10 BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the DNA sequence of the insert in a phage clone λ HC2211;
 Fig. 2 shows the DNA sequence of the insert in a phage clone λ HC2246;
 Fig. 3 shows the DNA sequence of the insert in a phage clone λ HC512, and the corresponding amino acid sequence;
 15 Fig. 4 shows the DNA sequence of the insert in a phage clone λ HC2206, and the corresponding amino acid sequence;
 Fig. 5 shows the DNA sequence of the insert in a phage clone λ HC2207, and the corresponding amino acid sequence;
 20 Fig. 6 shows the DNA sequence of the insert in a phage clone λ HC2216, and the corresponding amino acid sequence;
 Fig. 7 shows the DNA sequence of the insert in a phage clone λ HC2220, and the corresponding amino acid sequence;
 Fig. 8 shows the DNA sequence of the insert in a phage clone λ HC2230, and the corresponding amino acid sequence;
 25 Fig. 9 shows the DNA sequence of the insert in a phage clone λ HC2232, and the corresponding amino acid sequence;
 Fig. 10 shows the DNA sequence of the insert in a phage clone λ HC2244, and the corresponding amino acid sequence;
 30 Fig. 11 shows the DNA sequence of the insert in a phage clone λ HC2248, and the corresponding amino acid sequence;
 Fig. 12 shows the DNA sequence of the insert in a phage clone λ HC2256, and the corresponding amino acid sequence;
 Fig. 13 shows the DNA sequence of the insert in a phage clone λ HC2258, and the corresponding amino acid sequence;
 35 Fig. 14 shows the DNA sequence of the insert in a phage clone λ HC2270C, and the corresponding amino acid sequence;
 Fig. 15 shows the DNA sequence of the insert in a phage clone λ HC2410, and the corresponding amino acid sequence;
 40 Fig. 16 shows the DNA sequence of the insert in a phage clone λ HC2533, and the corresponding amino acid sequence;
 Fig. 17 shows the DNA sequence of the insert in a phage clone λ HC2607, and the corresponding amino acid sequence;
 Fig. 18 shows the DNA sequence of the insert in a phage clone λ HC2610, and the corresponding amino acid sequence;
 45 Fig. 19 shows the DNA sequence of the insert in a phage clone λ HC2211 as shown in Fig. 1, and the corresponding amino acid sequence;
 Fig. 20 shows the DNA sequence of the insert in a phage clone λ HC2246 as shown in Fig. 2, and the corresponding amino acid sequence;
 50 Fig. 21 is a schematic illustration of the construction of the expression plasmid pFETR3;
 Fig. 22 shows the structure of the plasmid pTRC24 with which cDNA of the phage clone 2207 has been integrated; and
 Fig. 23 shows the structure of the plasmid pFET42 with which cDNA of the phage clone 2246 has been integrated.

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BEST MODE OF CARRYING OUT THE INVENTION

The DNA coding for the blood-borne non-A, non-B hepatitis specific antigenic protein of the present

invention is cloned as follows:

Namely, the total RNA is prepared by dissolving a liver tissue in a guanidinium thiocyanate solution, extracting the mixture with phenol-chloroform and precipitating the RNA with isopropanol, according to the method of Chomczynski et al. [ANALYTICAL BIOCHEMISTRY, 162, 156 - 159 (1987)]. Alternatively, the
 5 total RNA is prepared by an ultra centrifugation of blood, and a portion of the total RNA thus obtained is purified by oligo(dT)cellulose column chromatography to isolate a poly A⁺ RNA.

The cDNA library is obtained with the total RNA or the poly A⁺ RNA as a template, by the random primer method described by Ebina et al., Cell, 40, 747 - 758 (1980). The construction of the cDNA library is accomplished by using a commercially available kit (Amersham Co.; cDNA Synthesis System Plus, cDNA
 10 Cloning System- λ gt 11). This kit utilizes an expression vector λ gt 11, and the cDNA is integrated into the β -gal gene on the λ gt 11 phage, and thus is easily expressed as the fused protein with β -galactosidase by the induction of a lactose operon promoter with isopropyl β -D-galactopyranoside (IPTG) or the like after infection of the phage with *Escherichia coli*.

The expression can be confirmed by the immunological screening method. This is conducted by
 15 coupling the serum of a patient suffering from the blood-borne non-A, non-B hepatitis, and an IgG fraction prepared therefrom as a 1st antibody, with an enzyme labelled 2nd antibody to develop a color [see Experimental Medicine, 6, 958 - 964 (1988) for the principle].

The positive clones thus obtained are further screened with serums from the patients suffering from hepatitis B and sera from healthy persons, to select a clone that specifically reacts with the serum from the
 20 patients suffering from non-A, non-B hepatitis.

The DNAs thus obtained encodes all or a part of the native protein of a blood-borne non-A, non-B hepatitis specific antigen, and the DNA of the present invention is not limited to the cDNAs but includes DNAs which encode the amino acid sequence of the protein via a different codon. The DNA of the present invention is not completely identical to the cDNA, from the viewpoint of their DNA sequences, but is
 25 homologous to the extent that it can be hybridized with the cDNA under the usual conditions used for the identification of viruses. The DNAs of the present invention also include DNAs coding for a protein having the aforementioned antigenicity.

The aforementioned DNA of the present invention is useful as a material for constructing a gene system which can be used for the production of a blood-borne non-A, non-B hepatitis specific antigen, in a host
 30 such as bacteria, yeast or animal cells etc. The bacterial host includes *Escherichia coli*. The required antigenic protein can be produced by a conventional genetic engineering method using the cDNA which has been cloned in the present invention. For example, an expression vector such as an expression plasmid can be constructed by adding a translational initiation codon and a translational termination codon upstream and downstream of the coding region of the cDNA according to the present invention, respectively, and
 35 inserting the obtained sequence to a vector such as a plasmid, comprising has an expression control system such as a promoter, a terminator or the like, functional in a selected host.

Promoter-terminator systems which can be used, include trp promoter, lac promoter, T7 promoter, rrnB terminator, and the like in *Escherichia coli*, and PGK promoter, ADH 1 promoter, GAL 10 promoter, ADH terminator, and the like in a yeast such as *Saccharomyces cerevisiae*. Also, there can be used SV40 early
 40 promoter, adenovirus major late promoter, Rous sarcoma virus LTR, SV40 poly A signal, and the like in an animal cell such as CHO, CV-1 and NIH3T3 cells. Conventional methods can be used for the construction of an expression vector, the transformation, the culture of a host, the induction of expression, and the recovery and purification of a produced protein. For example, the recovery and purification of a protein produced by
 45 *E. coli* can be carried out by homogenizing *E. coli* cells, dissolving insoluble matters containing a desired protein with 8M urea or the like, and subjecting to column chromatography on ion-exchange resin or the like. The production of the antigenic protein according to the present invention is specifically described in Example 7.

The DNA of the present invention can be used as a gene source for producing a live vaccine by integrating the DNA into a vector, such as vaccinia virus or the like.

50 The non-A, non-B hepatitis specific antigenic protein of the present invention is useful as a reagent for the diagnosis of non-A, non-B hepatitis when using a blood sample. For example, the 1st antibody of non-A, non-B hepatitis in the serum from a patient can be detected with the antigenic protein obtained by the process of the present invention, by methods such as the Western blot method, the enzyme immunoassay method, the latex agglutination method or the radioimmunoassay method, and thus an infection with blood-
 55 borne non-A, non-B hepatitis can be diagnosed. This has been confirmed by the successful results of the experimental detection of the 1st antibody in the serum from a patient suffering from non-A, non-B hepatitis with the antigenic protein prepared in Example 7 by the Western blot method.

The present invention is explained in more detail with reference to the following Examples.

Example 1 Construction of a cDNA library(1) Preparation of RNA

6 A non-cancerous tissue having a weight of ca. 1 g was obtained by an excision of liver cancer from a patient suffering from chronic blood-borne non-A, non-B hepatitis complicated with liver cancer. The total RNA was prepared from the tissue, by the method of Chomczynski et al. [ANALYTICAL CHEMISTRY, 162, 158 - 159 (1987)].

10 A 10 ml portion of the solution D [4 M guanidinium thiocyanate, 25 mM sodium citrate (pH 7), 0.5% sarcosyl, 0.1 M 2-mercaptoethanol] was added to about 1 g of each of the liver tissues derived from six patients, and each mixture was homogenized and solubilized. Then, to the solubilized products were sequentially added 1 ml of 2 M sodium acetate (pH 4), 10 ml of a water saturated-phenol, and 2 ml of chloroform/isoamyl alcohol (49 : 1), and the mixture was kept on ice for 15 minutes. The aqueous phase
15 was recovered by centrifuging the mixture at 12,000 rpm for 20 minutes at 4°C in a Sorvall ss-34 rotor, mixed with 10 ml of isopropanol and stood at -20°C for 1 hour. Then centrifugation was conducted at 12,000 rpm and 4°C for 20 minutes with a Sorvall SS-34 rotor, and the resulting precipitate was again dissolved in 3 ml of the solution D, mixed with 3 ml of isopropanol, and again stood at -20°C for 1 hour. The precipitate was recovered by centrifugation and washed with 75% ethanol, and the an amount of 0.5
20 mg - 1.5 mg of precipitate of the total RNA thus obtained was dissolved in distilled water.

The total RNA was prepared from blood by the following procedures to a 70 liter portion of plasma having an abnormal high ALT value and negative to HBsAg and HBV-DNA was added an equivalent amount of a diluent (50 mM Tris-HCl, 1 mM EDTA, pH 8.0), and the mixture was subjected to sucrose density gradient centrifugation at 90,000 x g to obtain a fraction having a specific gravity of 1.12 - 1.29. The fraction
25 was dialized against to the diluent, lyophilized, and then dissolved in a solution D containing guanidinium thiocyanate. After adding poly C as a carrier, the mixture was extracted with a mixture of phenol/chloroform/isoamyl alcohol, and to the aqueous phase was added an equivalent amount of isopropanol, to precipitate nucleic acid. After this procedure was repeated once more, the nucleic acid was stored in 75% ethanol, and further, was treated with a RNase free DNase fraction which had been removed
30 a potentially contaminated RNase in a trace amount by affinity chromatography of a commercially available RNase free DNase on agarose-5'-(4-aminophenylphosphoryl)-uridine-2 (3')-phosphate, to remove DNA incorporated in the RNA fraction. Further, the poly C as a carrier in the remaining RNA was removed with an oligo (dG)-cellulose column and purified with NENSORB (DuPont Co.).

The poly A⁺ RNA was prepared in the following manner. To a solution containing ca. 500 µg of the total
35 RNA was added 20% sodium laurylsulfate to adjust to 0.5%, and the mixture was heated at 65°C for 10 minutes. After the adjustment of the mixture to 10 mM Tris-HCl (pH 8), 0.5 M NaCl and 1 mM of EDTA, the mixture was subjected to oligo(dT)cellulose (Pharmacia Co.) column chromatography. Thereafter, elution with a solution comprising 10 mM Tris-HCl (pH 7.5) and 1 mM EDTA produced a poly A⁺ RNA, in a yield of 10 - 15 µg.

(2) Synthesis of cDNA

cDNA was synthesized with a commercially available cDNA synthesizing kit [Amersham Co.; cDNA
45 Synthesis System Plus. (code: RPN 1256)], and to 5 µg of the RNA prepared above were added 10 µl of 5 x the first strand synthesis reaction buffer, 2.5 µl of a sodium pyrophosphate solution, 2.5 µl of human placenta ribonuclease inhibitor, 5 µl of a deoxynucleoside triphosphate mixture, 5 µl of a primer, 2 µl of [α -³²P]dCTP (Amersham PB 10205), water and 100 units of a reverse transcriptase solution, to a total volume of 50 µl. As the primer, an oligo(dT)primer was used for RNA Nos. 4 and 5 as template, and a random
50 hexanucleotide primer was used for other RNAs. After incubation at 42°C for 40 minutes, to the first strand cDNA synthesis reaction mixture were added 93.5 µl of the second strand synthesis reaction buffer, 4 units of *E. coli* ribonuclease H, 115 units of *E. coli* DNA polymerase I and water to a total volume of 250 µl. After reaction at 12°C for 60 minutes and at 22°C for 60 minutes, the reaction mixture was incubated at 70°C for 10 minutes. Then, after adding 10 units of T4 DNA polymerase and incubating 37°C for 10
55 minutes, 10 µl of 0.25 M EDTA (pH 8.0) was added. The reaction mixture was extracted with phenol/chloroform, and after adding a 4 M ammonium acetate solution in an equivalent amount, subjected to ethanol precipitation. The cDNAs shown in Table 1 were obtained by repeating the above-described procedures. Note, the RNA sample Nos. 4, 5, 22, 24 and 25 are derived from liver cells and No. 28 is

derived from blood.

Table 1

RNA Sample	Amount of RNA (μ g)	Double Strand cDNA (ng)
No. 4 (poly A ⁺ RNA)	15	1260
5 (poly A ⁺ RNA)	10.5	4500
22 (total RNA)	8	260
24 (total RNA)	20	1400
25 (total RNA)	22	260
26 (total RNA)	5	5200

(3) Construction of cDNA library

The cDNA library was constructed using a cDNA Cloning System- λ gt 11 (Amersham code RPN 1280), and to the cDNA obtained above (ca. 1 μ g) were added 4 μ l of the M buffer, 2 μ l of 1 x SAM solution, water, and 20 units of EcoR I methylase, to a total volume of 20 μ l. After reaction at 37 $^{\circ}$ C for 60 minutes, the reaction mixture was heated at 70 $^{\circ}$ C for 10 minutes and then 3 μ l of L buffer, 2 μ l of a EcoR I linker, water, and 5 units of T4 DNA ligase were added, to a total volume of 30 μ l, and the mixture allowed to react at 15 $^{\circ}$ C overnight. After terminating the reaction by heating at 70 $^{\circ}$ C for 10 minutes, 10 μ l of the E buffer, water, and 100 units of EcoR I were added to a total volume of 100 μ l, and the mixture allowed to react at 37 $^{\circ}$ C for 5 hours. After terminating the reaction by heating at 70 $^{\circ}$ C for 10 minutes, free linkers were removed with a column equipped in the cDNA cloning system, to yield the EcoR I linker coupled cDNAs in the amounts shown in Table 2.

Table 2

RNA Sample	EcoR I linker coupled cDNA (ng)
No. 4 (poly A ⁺ RNA)	460
5 (poly A ⁺ RNA)	1470
22 (total RNA)	27
24 (total RNA)	100
25 (total RNA)	24
26 (total RNA)	2200

To 10 - 100 ng of the cDNA were added 1 μ g of the λ gt 11 arm, 1 μ g of the L buffer, water, and 2.5 units of T4 DNA ligase, to a total volume of 10 μ l, and the mixture allowed to react at 15 $^{\circ}$ C overnight. To this reaction mixture were added 10 μ l of Extract A and 15 μ l of Extract B, and the mixture was kept at 20 $^{\circ}$ C for 2 hours to carry out in vitro packaging. Then, to the mixture were added 0.5 ml of SM buffer (50 mM Tris-HCl, pH 7.5, 100 mM NaCl, 10 mM MgSO₄, 0.01% gelatin), and several drops of chloroform, to obtain a phage solution. The phage solution was titrated, and the results shown in Table 3 below were obtained as the cDNA libraries.

Table 3

RNA Sample	Recombinant Phage Number (PFU)	Recombination Rate (%)
No. 4 (poly A ⁺ RNA)	1.2 x 10 ⁵	75
5 (poly A ⁺ RNA)	3.2 x 10 ⁶	82
22 (total RNA)	3.0 x 10 ⁵	48
24 (total RNA)	1.3 x 10 ⁶	48
25 (total RNA)	2.0 x 10 ⁵	53
26 (total RNA)	5.1 x 10 ⁷	89

Recombination rate = Recombinant phage number/total phage number x 100

Example 2 Preparation of a first antibody for the screening of the cDNA libraries

E. coli Y1090 strain was incubated with shaking in an L-broth (10 g/l bacto-trypton, 5 g/l bacto-yeast extract and 10 g/l NaCl) containing 0.4% maltose and 50 µg/ml ampicillin. Then, one ml portion of the culture was added to 50 ml of the L-broth containing 0.4% maltose and ampicillin (50 µg/ml), and the mixture was incubated with shaking at 37°C until OD₆₀₀ reached 0.5 (2.5 x 10⁸ cells/ml). *E. coli* was collected by centrifugation and suspended in 5 ml of Phosphate buffered-saline (PBS). A 6 µl of 0.5 M EDTA (pH 8) and lysozyme (final concentration: 0.1 mg/ml) were added, and the mixture was kept on ice for 30 minutes. *E. coli* lysate was obtained by repeating freezing and thawing three times.

The 1st antibody was obtained by the procedure described below. Sera of 5 convalescents from acute non-A, non-B hepatitis and sera of 5 patients suffering from chronic non-A, non-B hepatitis were used together as the serum from patients with blood-borne non-A, non-B hepatitis. A 10 ml portion of the serum was treated in 33% saturated ammonium sulfate to give a precipitate containing immunoglobulin, the precipitate was suspended in 10 ml of TBS [10 mM Tris-HCl (pH 7.5), 150 mM NaCl], 10 ml of the aforementioned *E. coli* lysate was added, and the mixture was shaken at 4°C overnight or at 37°C for 1 hour. After removing the precipitate by centrifugation at 3,000 rpm for 10 minutes (HITACHI 05PR-22), 180 ml of TBS containing 1% gelatin was added, and the mixture was filtered with MILLEX-HA (0.45 µm, Millipore Co.) to give a 1st antibody.

For the serum from healthy people and the serum from a patient suffering from hepatitis B, 1 ml of the *E. coli* lysate was added to 1 ml of each serum, and the mixture was shaken at 4°C overnight. After removing the precipitate by centrifugation at 3,000 rpm for 10 minutes (HITACHI 05PR-22), 18 ml of TBS containing 1% gelatin was added, and the mixture was filtered with MILLEX-HA (0.45 µm, Millipore Co.) to give a 1st antibody.

Example 3 Screening of cDNA libraries

After the *E. coli* Y1090 strain was cultured in 10 ml of L-broth containing 0.4% maltose and ampicillin (50 µg/ml) at 37°C overnight, collected by centrifugation and suspended in 4 ml of 10 mM MgSO₄ to give a cell for plating. The phage solution was diluted with an SM buffer to give a concentration of ca. 6,000 PFU/100 µl and 200 µl of the cell for plating and 100 µl of the phage solution were combined and maintained at 37°C for 15 - 20 minutes. The solution was added to 10 ml of L-top agar [L-broth containing agarose (7 g/l)] and poured into a plate (EIKEN CHEMICAL CO., LTD.: No. 2 type square schale) containing L-agar (L-broth containing 15 g/l bacto-agar). After culturing at 43°C for 3 - 4 hours, a nitrocellulose filter (Schleicher & Schnell, BA85) impregnated with 10 mM IPTG (isopropyl β-D-thiogalactopyranoside) and air-dried was layered on the plate, and culturing was continued further at 37°C for 3 - 4 hours. The filter was removed and washed with TBS (10 mM Tris-HCl, pH 7.5, 150 mM NaCl) and shaken in TBS containing 5% skimmed milk (Snow Brand Milk Products Co., Ltd.) at room temperature for 1 - 2 hours. The filter was washed by shaking in TBS for 1 - 2 minutes. After repeating these procedures, the filter was dipped in the aforementioned 1st antibody, and the reaction was conducted at 4°C overnight. After washing the filter five times in TBST (TBS containing 0.05% Tween 20) for 5 minutes, it was dipped into a peroxidase conjugated anti-human IgG (goat) (Cappel Co.; code 3201-0081) solution (500-fold dilution with TBS containing 1%

gelatin), to conduct the reaction at room temperature for 1.5 hours. The filter was then washed with TBST in the same manner as described above, and was reacted with a HRP-color solution [120 mg HRP-color (Bio-RAD Co.) in 40 ml of methanol, 200 ml of TBS and 120 μ l of hydrogen peroxide], and the colored clone was judged positive. As a result, the positive clones as shown in Table 4 were obtained.

Table 4

RNA Sample	Treated clone Number	Positive clone Number
No. 4	340,000	5
5	270,000	8
22	150,000	45
24	300,000	14
25	200,000	18
26	260,000	9

Single plaque isolation was conducted for the positive clones thus obtained, and their reactivities with the serum derived from healthy subjected and the serum derived from the patient suffering from hepatitis B was examined.

As a result of the reaction with the 1st antibodies derived from 5 normal subjects and 5 patients with hepatitis B in the same manner as described above, 61 clones were obtained which reacted specifically with the serum derived from patients with blood-borne non-A, non-B hepatitis. These clones (phages) are shown in Table 5.

In this connection, *E. coli* Y1090 strains containing these clones have been deposited with the Agency of Industrial Science and Technology, Fermentation Research Institute, Japan (address: 1-3, Higashi 1-Chome, Tsukuba, Ibaragi, Japan), and some of these strains were transferred to international deposit based on the Budapest Treaty, on June 14, 1990.

Table 5

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)	Deposit Date
5				
10	λHC 432	10897		1987 7 26
	λHC 436	10898		1989 7 26
	λHC 512	10841	2951	1989 7 13
15	λHC 522	10842		1989 7 13
	λHC 524	10843		1989 7 13
20	λHC 526	10844		1989 7 13
	λHC 2206	10845	2952	1989 7 13
	λHC 2207	10846	2953	1989 7 13
25	λHC 2211	10876	2956	1989 7 21
	λHC 2216	10877	2957	1989 7 21
30	λHC 2217	10852		1989 7 18
	λHC 2220	10853	2954	1989 7 18
	λHC 2225	10854		1989 7 18
35	λHC 2230	10916	2966	1989 8 2
	λHC 2232	10930	2968	1989 8 9
40	λHC 2239	10931		1989 8 9
	λHC 2240	10855		1989 7 18
	λHC 2241	10856		1989 7 18
45	λHC 2242	10857		1989 7 18
	λHC 2243	10878		1989 7 21
50	λHC 2244	10879	2958	1989 7 21
	λHC 2246	10858	2955	1989 7 18

55

Table 5 (continued)

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)	Deposit Date		
5						
10	λHC 2248	10880	2959	1989	7	21
	λHC 2249	10917		1989	8	2
	λHC 2250	10904		1989	7	28
15	λHC 2252	10881		1989	7	21
	λHC 2255	10889		1989	7	26
20	λHC 2256	10890	2960	1989	7	26
	λHC 2558	10891	2961	1989	7	26
	λHC 2259	10892		1989	7	26
25	λHC 2263	10893		1989	7	26
	λHC 2264	10932		1989	8	9
30	λHC 2265	10933		1989	8	9
	λHC 2268	10894		1989	7	26
	λHC 2270	10895	2962	1989	7	26
35	λHC 2271	10896		1989	7	26
	λHC 2404C	10899		1989	7	26
40	λHC 2405B	10900		1989	7	26
	λHC 2410A	10905		1989	7	28
	λHC 2410C	10918	2967	1989	8	2
45	λHC 2410D	10934		1989	8	9
	λHC 2413	10919		1989	8	2
50	λHC 2414A	10906		1989	7	28
	λHC 2424A	10911		1989	7	28

Table 5 (continued)

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)	Deposit Date		
5						
10	λHC 2501	10920		1989	8	2
	λHC 2502	10847		1989	7	13
	λHC 2505	10921		1989	8	2
15	λHC 2507	10935		1989	8	9
	λHC 2508	10859		1989	7	18
20	λHC 2509	10936		1989	8	9
	λHC 2512	10882		1989	7	21
	λHC 2514	10860		1989	7	18
25	λHC 2516	10861		1989	7	18
	λHC 2533	10907	2963	1989	7	28
30	λHC 2534	10937		1989	8	9
	λHC 2535	10883		1989	7	21
	λHC 2602	10908		1989	7	28
35	λHC 2603B	10922		1989	8	2
	λHC 2607	10909	2964	1989	7	28
40	λHC 2608	10923		1989	8	2
	λHC 2610	10910	2965	1989	7	28

45

Example 4 DNA sequence of the cDNA inserted into the phage clone λHC2211

50 The recombinant phage λHC2211 was proliferated in the *E. coli* Y1090 strain, the phage was purified by a conventional method (Experimental Medicine, Vol. 5, 994 - 998, 1987), and the phage DNA was prepared by a treatment with sodium lauryl sulfate and phenol. An amount of ca. 100 μg of the phage DNA was treated with EcoR I, and ca. 0.6 μg of a DNA fragment having ca. 700 base pairs (bp) as a cDNA was recovered by 1% low melting agarose (Biolad Co.) gel electrophoresis. This DNA fragment was integrated

55 at the EcoR I site in a phage vector M13mp18 (TAKARA SHUZO), and further inserted at the EcoR I site in a plasmid pUC19 (TAKARA SHUZO), to give pMC26. Next, an EcoR I-ended cDNA fragment was prepared from the pMC26, treated with Bal I, and inserted to the Hinc II site and the Hinc II-EcoR I site of M13mp18. Also, the EcoR I-ended cDNA fragment was treated with Sau3A I and then inserted to the BamH I-EcoR I

site of M13mp18. The DNA sequence of the cDNA was determined by the dideoxy method (J. Messing, *Methods in Enzymology*, 101, 20 - 78, 1983) using a recombinant phage containing the M13mp18 thus obtained as a vector. The DNA sequence is shown in Fig. 1.

The blood-borne non-A, non-B virus is believed from its property to be a flavivirus [Qui-Lim Choo et al., *Science*, 244, 359 (1989)]. A protein derived from the flavivirus is synthesized as a precursor polypeptide from a serial long open reading frame [E.G. Westaway, *Advances in virus research*, 33, 45 (1987)]. On the other hand, the synthesis of the protein, which will be presumably synthesized from the 5'-end of the DNA sequence shown in Fig. 1, is terminated on the way of the cDNA by the presence of a terminating codon. Considering cDNA inserted to λ HC2211 to be derived from the blood-borne non-A, non-B hepatitis virus which is a flavivirus, it can be assumed as an inevitable possibility in the construction of the cDNA library that two DNA fragments have been integrated at the same time. It can be also considered that the region specific to non-A, non-B hepatitis in λ HC2211 may be at least a part of a protein portion in front of the terminating codon.

15

Example 5 DNA sequence of the cDNA inserted into the phage clone λ HC2246

The phage DNA was prepared from the recombinant phage λ HC2246 in the same manner as in Example 4. Approximately 10 μ g of the phage DNA was treated with Kpn I and Sac I, and blunt-ended with a Klenow fragment of *E. coli* DNA polymerase I. About 0.3 μ g of a DNA fragment having ca. 2.5 kilo base pairs (kb) was recovered by 1% low melting agarose (Biolad Co.) gel electrophoresis, and integrated at the Sma I site in a phage vector M13mp18 (TAKARA SHUZO). This DNA fragment was also inserted into the Sma I site of a plasmid pUC18 (TAKARA SHUZO) to give pMC42. Next, about 20 μ g of pMC42 was treated with EcoR I and Pvu II, and about 2 μ g of the DNA fragment having ca. 0.5 kb and containing the cDNA was recovered by 1% low melting agarose (Biolad Co.) gel electrophoresis. The EcoR I-Pvu II DNA fragment was treated with Bal I, and inserted into the EcoR I-Hinc II site and the Hinc II site of M13mp18, respectively. Using the recombinant phage on M13mp18 vector, the DNA sequence of the cDNA was determined by the dideoxy method with a Lambda gt11 primer (New England Biolad Co.) or an M13 primer (TOYO BOSEKI) (J. Messing, *Methods in Enzymology*, 101, 20 - 78, 1983). The DNA sequence is shown in Fig. 2.

Example 6 DNA sequences of cDNA inserted into phage λ HC512, λ HC2206, λ HC2207, λ HC2216, λ HC2220, λ HC2230, λ HC2232, λ HC2244, λ HC2248, λ HC2256, λ HC2258, λ HC2270, λ HC2410c, λ HC2533, λ HC2607 and λ HC2610

The phage DNAs were prepared in the same manner as in Example 4 from the recombinant phages λ HC512, λ HC2206, λ HC2207, λ HC2216, λ HC2220, λ HC2230, λ HC2232, λ HC2244, λ HC2248, λ HC2256, λ HC2258, λ HC2270, λ HC2410c, λ HC2533, λ HC2607 and λ HC2610.

The EcoR I fragments containing the cDNA of λ HC2206 and λ HC2232 were prepared in the same manner as Example 4, and inserted into the EcoR I site of M13mp18 and pUC19, respectively. On the other hand, the Kpn I-Sac I fragments containing cDNA of λ HC512, λ HC2207, λ HC2216, λ HC2220, λ HC2230, λ HC2244, λ HC2248, λ HC2256, λ HC2258, λ HC2270, λ HC2410c, λ HC2533, λ HC2607 and λ HC2610 were prepared in the same manner as in Example 5, and the DNA fragments from λ HC2230, λ HC2256, λ HC2270, λ HC2410c, λ HC2533, λ HC2607 and λ HC2610 were inserted into the Sma I site of pUC18, the DNA fragments from λ HC512, λ HC2207, λ HC2216, λ HC2220 and λ HC2244 were inserted to the Hinc II site of pUC19, and the DNA fragments from λ HC2248 and λ HC2258 were inserted to the Kpn I-Sac I site of pUC19, respectively. Further, the Hinc II-Cla I fragment containing cDNA was recovered from the plasmid to which the DNA fragment of λ HC2244 had been inserted, and inserted to the Hinc II-Cla I site of M13mp18. Using the obtained plasmids and phages, the DNA sequences of the cDNAs were determined by the dideoxy method with a Lambda gt11 primer (New England Biolabs Co.) or an M13 primer (TOYO BOSEKI) (J. Messing, *Methods in Enzymology*, 101, 20 - 78, 1983). Further, oligonucleotides having the corresponding sequence to a part of the DNA sequence of the obtained cDNA were synthesized by an automatic DNA synthesizer (380A/APPLIED BIOSYSTEMS CO.). The DNA sequences of the cDNAs were also determined by the dideoxy method using the synthetic oligonucleotides as a primer.

The determined DNA sequences of the cDNAs are shown in Figs. 3 - 18, respectively.

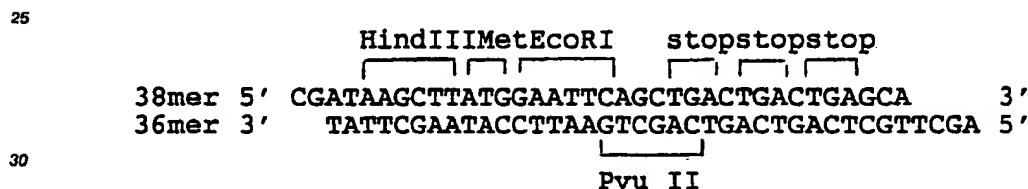
Example 7 Expression of the cDNAs coding for the blood-borne non-A, non-B hepatitis specific antigenic protein in E. coli

5 (1) Construction of the expression vector pFETR3 (Fig. 21)

Plasmid pTM1 wherein the 331 bp DNA fragment containing a tryptophan (trp) promoter from the Hpa II site 310 bp upstream of the transcriptional initiation site to the Taq I site 21 bp downstream of the transcriptional initiation site of the E. coli trp operon, prepared from trp transducing phage λ cl857 trpED10
 10 [G.F. Miozzari et al., J. Bacteriology, 133, 1457 (1978)] had been inserted into the Cla I site of pBR322, was digested with EcoR I and Hind III, and ca. 0.4 kb DNA fragment containing the trp promoter was recovered by low-melting agarose gel electrophoresis. pKK223-3 (Pharmacia Co.) was digested with EcoR I and Hind III to give a 4.5 kb DNA fragment, to which the aforementioned ca. 0.4 kb DNA fragment was then
 15 ligated using T4 DNA ligase. The plasmid thus obtained was digested with EcoR I and blunted with the E. coli DNA polymerase I (Klenow fragment), and digested with Pvu II. The ca. 3 kb DNA fragment thus obtained was cyclized using the T4 DNA ligase to give a plasmid pFETR1.

The plasmid pFETR1 was digested with EcoR I, made the ends of the DNA fragment were blunted with the E. coli DNA polymerase I (Klenow fragment) and then cyclized using T4 DNA ligase, to give a plasmid pFETR12 containing trp promoter wherein the EcoR I site had been deleted.

20 To give the translational initiation codon (ATG) and the termination codon (TGA) and the cloning site downstream of the trp promoter on the plasmid pFETR12, oligonucleotides of 36-mer and 38-mer were synthesized by an automatic DNA synthesizer (380A/APPLIED BIOSYSTEMS CO.) and annealed to give the following DNA linker.



To the DNA fragment obtained by digesting the aforementioned plasmid pFETR12 with Cla I and Hind III was ligated the aforementioned synthetic DNA linker using the T4 DNA ligase, to give an expression
 35 vector pFETR3 containing a trp promoter.

(2) Expression of cDNA in the recombinant phage λ HC2207 in E. coli

40 As described in Example 6, the plasmid (referred to as pMC24 hereinafter) obtained by inserting the cDNA of λ HC2207 (Fig. 5) into the Hinc II site of pUC19 was digested with Pst I and EcoR I, and the about 0.8 kb DNA fragment containing cDNA was obtained by low-melting agarose gel electrophoresis. Since this DNA fragment has been deleted a part of the 5'-end of the cDNA, oligonucleotides of 79 mer and 73 mer were synthesized on the basis of the amino sequence encoded by the cDNA portion corresponding to the
 45 deleted region using the DNA synthesizer (380A/APPLIED BIOSYSTEMS CO.), phosphorylated with T4 polynucleotide kinase, and then annealed to give the following DNA linker:

50

55

25 The cells were collected by centrifugation, suspended in a buffer containing 2% sodium dodecylsulfate (SDS) and 500 mM 2-mercaptoethanol, solubilized by boiling, and subjected to SDS-polyacrylamid gel electrophoresis in the conventional manner. The proteins were blotted on a nitrocellulose filter using a semidry blotting apparatus (ATTO Co.), and the reacted with the antibody prepared from the serum of the patient with non-A, non-B hepatitis as described in Example 3. As a result, it was confirmed that the
30 expression product reacted with the antibody.

57mer 5' CTAGAAATAATTTTGTTTAACTTTAAGAAGGAG
57mer 3' TTTATTAAAACAAATTGAAATTCTTCCTC

50

Met EcoR I Hpa I

ATATACATATGGAATTCGTTAACA 3'

TATATGTATACCTTAAGCAATTGTTCGA 5'

pFETR342 was digested with EcoR I and Hind III and subjected to low-melting agarose gel elec-

trophoresis, to give the ca. 0.5 kb DNA fragment containing the cDNA and the translational termination codon. On the other hand, a DNA fragment was obtained by digesting pFET710 with EcoR I and Hind III. This DNA fragment and the ca. 0.5 kb DNA fragment were ligated using T4 DNA ligase, to give an expression vector pFET42 containing a T7 promoter and λ HC2246 cDNA under the control of said promoter. The structure of the vector is shown in Fig. 23.

The E. coli JM109 (DE3) strain (PROMEGA Co.), wherein the expression of the T7 RNA polymerase can be induced with IPTG, was transformed with pFET42. The transformed strain was inoculated in the L medium (1% bacto-trypton, 0.5% yeast extract, 0.5% NaCl) containing ampicillin (50 μ g/ml) and cultured by shaking at 30 °C for 12 - 18 hours. A 1 ml portion of the culture was inoculated in 100 ml of the L medium containing ampicillin (50 μ g/ml), and subjected to shake culture at 30 °C. When A_{660} reached ca. 0.3, 0.5 mM IPTG was added, and the culture was further continued for 3 - 5 hours. The bacterial cell obtained was treated in the same manner as described above (2), and it was confirmed that the expression product reacted with the antibody prepared from the serum of the patient with non-A, non-B hepatitis.

(4) The expression of cDNA in λ HC2207 and cDNA in λ HC2246 in E. coli was confirmed in the above-mentioned (2) and (3), and it is apparent that any cDNAs in other λ HC recombinant vectors can be expressed to give an expression product thereof.

As illustrated in (2) and (3), the expression products of the cDNAs in λ HC2207 and λ HC2246 clones obtained in Example 3 reacted with the serum of the patient with non-A, non-B hepatitis, as when using the recombinant phage in Example 3. Therefore, it has been confirmed that the expression product of the DNA which encodes a non-A, non-B hepatitis specific antigenic protein according to the present invention can be used for the detection of an antibody to a non-A, non-B hepatitis specific antigen.

Industrial Applicability

The DNA coding for the blood-borne non-A, non-B hepatitis specific antigenic protein according to the present invention is useful as a gene for producing said antigen. Also, the antigenic protein as the expression product of the gene reacts with an antibody in serum against the hepatitis specific antigen, therefore, said antigenic protein is useful as a reagent for the diagnosis of the presence of the antibody in the serum of a subject.

Claims

1. A DNA coding for a blood-borne non-A, non-B hepatitis specific antigenic protein which appears in a human liver cell and/or blood on the pathopoiesis of the blood-borne non-A, non-B hepatitis.
2. A DNA according to claim 1, wherein said DNA is a cDNA corresponding to RNA extracted from the liver cell of a human patient suffering from the blood-borne non-A, non-B hepatitis.
3. A DNA according to claim 1, wherein said DNA is the cDNA corresponding to RNA extracted from the blood of a human patient suffering from the blood-borne non-A, non-B hepatitis.
4. A DNA according to claims 2 or 3, wherein said DNA is a cDNA inserted to the following phage clone, or contains said cDNA:

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	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)
5	λHC 432	10897	
	λHC 436	10898	
10	λHC 512	10841	2951
	λHC 522	10842	
15	λHC 524	10843	
	λHC 526	10844	
20	λHC 2206	10845	2952
	λHC 2207	10846	2953
	λHC 2211	10876	2956
25	λHC 2216	10877	2957
	λHC 2217	10852	
30	λHC 2220	10853	2954
	λHC 2225	10854	
	λHC 2230	10916	2966
35	λHC 2232	10930	2968
	λHC 2239	10931	
40	λHC 2240	10855	
	λHC 2241	10856	
	λHC 2242	10857	
45	λHC 2243	10878	
	λHC 2244	10879	2958
50	λHC 2246	10858	2955

55

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)
5	λHC 2248	10880	2959
10	λHC 2249	10917	
	λHC 2250	10904	
	λHC 2252	10881	
15	λHC 2255	10889	
	λHC 2256	10890	2960
20	λHC 2258	10891	2961
	λHC 2259	10892	
	λHC 2263	10893	
25	λHC 2264	10932	
	λHC 2265	10933	
30	λHC 2268	10894	
	λHC 2270	10895	2962
	λHC 2271	10896	
35	λHC 2404C	10899	
	λHC 2405B	10900	
40	λHC 2410A	10905	
	λHC 2410C	10918	2967
	λHC 2410D	10934	
45	λHC 2413	10919	
	λHC 2414A	10906	
50	λHC 2424A	10911	

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)
5	λ HC 2501	10920	
	λ HC 2502	10847	
10	λ HC 2505	10921	
	λ HC 2507	10935	
15	λ HC 2508	10859	
	λ HC 2509	10936	
	λ HC 2512	10882	
20	λ HC 2514	10860	
	λ HC 2516	10861	
25	λ HC 2533	10907	2963
	λ HC 2534	10937	
	λ HC 2535	10883	
30	λ HC 2602	10908	
	λ HC 2603B	10922	
35	λ HC 2607	10909	2964
	λ HC 2608	10923	
40	λ HC 2610	10910	2965

5. A DNA coding for an amino acid sequence encoded by the DNA according to claims 2 or 3 with a different codon.

6. A DNA having a nucleotide sequence according to any one of Figs. 1 - 18.

45 7. A DNA coding for an amino acid sequence according to any one of Figs. 3 - 20.

8. A blood-borne non-A, non-B hepatitis specific antigenic protein which appears in a human liver cell and/or blood on the pathopoiesis of the blood-borne non-A, non-B hepatitis, characterized by being produced with a DNA coding for said protein by a genetic recombination technique.

9. A protein according to claim 8, wherein said protein has an amino acid sequence described in any one of 50 Figs. 3 - 20.

10. A process for producing a blood-borne non-A, non-B hepatitis specific antigenic protein which appears in a human liver cell and/or blood on the pathopoiesis of the blood-borne non-A, non-B hepatitis, characterized in that a host transformed with an expression vector containing a DNA coding for said protein is cultured.

55 11. A process according to claim 10, wherein said expression vector is a plasmid and said host is Escherichia coli.

12. A recombinant DNA molecule for use in the cloning of DNA in bacteria, yeast or animal cells, which is (a) a cDNA inserted into the phage clones listed below;

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(b) a DNA which can be hybridized with said cDNA and encodes a blood-borne non-A, non-B hepatitis specific antigenic protein; or

(c) a DNA coding for an amino acid sequence encoded by the DNA described in said (a) or (b) with a different codon:

5

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)
10			
	λHC 432	10897	
	λHC 436	10898	
15	λHC 512	10841	2951
	λHC 522	10842	
20	λHC 524	10843	
	λHC 526	10844	
	λHC 2206	10845	2952
25	λHC 2207	10846	2953
	λHC 2211	10876	2956
30	λHC 2216	10877	2957
	λHC 2217	10852	
	λHC 2220	10853	2954
35	λHC 2225	10854	
	λHC 2230	10916	2966
40	λHC 2232	10930	2968
	λHC 2239	10931	
	λHC 2240	10855	
45	λHC 2241	10856	
	λHC 2242	10857	
50	λHC 2243	10878	
	λHC 2244	10879	2958
55	λHC 2246	10858	2955

	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)
5	λHC 2248	10880	2959
	λHC 2249	10917	
10	λHC 2250	10904	
	λHC 2252	10881	
15	λHC 2255	10889	
	λHC 2256	10890	2960
	λHC 2258	10891	2961
20	λHC 2259	10892	
	λHC 2263	10893	
25	λHC 2264	10932	
	λHC 2265	10933	
	λHC 2268	10894	
30	λHC 2270	10895	2962
	λHC 2271	10896	
35	λHC 2404C	10899	
	λHC 2405B	10900	
	λHC 2410A	10905	
40	λHC 2410C	10918	2967
	λHC 2410D	10934	
45	λHC 2413	10919	
	λHC 2414A	10906	
50	λHC 2424A	10911	

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	Phage Clone No.	National Deposit No. (FERM P.)	International Deposit No. (FERM BP.)
5	λHC 2501	10920	
	λHC 2502	10847	
10	λHC 2505	10921	
	λHC 2507	10935	
15	λHC 2508	10859	
	λHC 2509	10936	
	λHC 2512	10882	
20	λHC 2514	10860	
	λHC 2516	10861	
25	λHC 2533	10907	2963
	λHC 2534	10937	
	λHC 2535	10883	
30	λHC 2602	10908	
	λHC 2603B	10922	
35	λHC 2607	10909	2964
	λHC 2608	10923	
40	λHC 2610	10910	2965

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SEQUENCE LISTING

SEQ ID NO.: 1

SEQUENCE TYPE: Nucleotide

SEQUENCE LENGTH: 668 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAATTCCTTCA CGGAATTGGA TGGGGTGC GG CTACACAGGT ACGCTCCGGC 50
GTGCAAGCCT CTCCTACGGG ATGAGGTCAC ATTCCAGGTC GGGCTCAACC 100
AATTCCTCGGT TGGGTCACAG CTCCCATGTG AACCCGAACC GGATGTAATG 150
GTGGTCACCT CTATGCTCAC CGACCCCTCC CATATTACAG CAGAGACGGC 200
TAAGCGTAGG CTGGCCAGAG GGTCTCCCCC TTCTTTGGCC AGCTCTTCAG 250
CTAGTCAGTT GTCTGCGCCC TCCTTGAAGG CGACATGCAC CACCCGTCAT 300
GACTCCCCGG ACGCTGACCT CATAGAGGCC AACCTCCTGT GGCGGCAGGA 350
GATGGGCGGG AACATCACCC GTGTGGAGTC AGAGAATAAG GTAGTGATTT 400
TGGACTCTTT TGAACCGCTT CGGGTGGAGG AGGATGAGAG GGAAGTATCC 450
GTAGCGGCGG ATTTCAAGTGA CTTGAATGCA GAATGAATCC CGTGGCTCAC 500
TTCCTAGACT ATTTGCCAAA GAAGATGTTG CCTGGCCAT GATCAAGATG 550
ACACAAACGG TGGCCTTTTG CAGGGAGAAC CGCCGTGGAG GCCTGTGTCT 600
GTGGCACTGG TAGCTTCTCT CTGCAGGCAA AGACCCCATG GCTTAGTTCT 650
TCATCAGAGT GAGAATTC 668

SEQ ID NO.: 2

SEQUENCE TYPE: Nucleotide

SEQUENCE LENGTH: 479 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

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GAATTCTTCA CGGAGTTGGA TGGGGTACGG CTGCACAGGT ACGCTCCGGC 50
GTGCAAGCCA CTCCTACGGG ATGAGGTCAC ATTCCAGGTC GGGCTCAACC 100
AATTTCCAGT TGGATCACAG CTCCCATGTG AGCCCGAGCC GGATGTAGCG 150
GTGCTCACTT CCATGCTCAC CGACCCCTCC CACATTACAG CAGAGACGGC 200
TAAGCGTAGG CTGGCCAGGG GGTCCCCCCC CTCCTTGGCC AGCTCTTCAG 250
CTAGTCAGTT GTCTGCGCCC TCCTTGAAGG CGACATGCAC TACCCACCAT 300
GACTCCCCGG ACGCTGACCT CATCGAGGCC AACCTCCTGT GCGGGCAGGA 350
GATGGGAGGA AACATCACCC GCGTGGAGTC AGAGAATAAG GTAGTAATTC 400
TAGACTCTTT TGACCCGCTC CGAGCGGAGG AGGATGAGAG GGAAGTGTCC 450
GTTGCGGCGG AGATCCTGCG GAAGACCAG                                479

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SEQ ID NO.: 3

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 498 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

TCA CTC AAT CCT CGA CGG TGC TGC CGG TGC GGC AAT CCG	39
Ser Leu Asn Pro Arg Arg Cys Cys Arg Cys Gly Asn Pro	
5 10	
GAA CGA TAC CGA CGC CGG ATC GCC CTG CTG CCC CCA CGC	78
Glu Arg Tyr Arg Arg Arg Ile Ala Leu Leu Pro Pro Arg	
15 20 25	
ATT TAC CGC CCG GAC TGT CAG CCT GTA GTT CCC CAG CGC	117
Ile Tyr Arg Pro Asp Cys Gln Pro Val Val Pro Gln Arg	
30 35	
CAG TTG CGT GAA GCG GTA TGT GGT TTC CGT CGT CCG GGC	156
Gln Leu Arg Glu Ala Val Cys Gly Phe Arg Arg Pro Gly	
40 45 50	
CGT GCT GAC CAG CCG CTC ACT GCC GTC GTC CGT GTT ACG	195
Arg Ala Asp Gln Pro Leu Thr Ala Val Val Arg Val Thr	
55 60 65	
GTC AGA CGG AGC AGG AAA CTC ACG CCT TCA CAC TTC GGT	234
Val Arg Arg Ser Arg Lys Leu Thr Pro Ser His Phe Gly	
70 75	
GTG TCC CAT CGC GCC AGC ACC TGATATCCCC CGCTGTCTGC	275
Val Ser His Arg Ala Ser Thr	
80 85	
AGTGACTTCT GCGGTCAGGT GCTGCACCGC TCGTGACACC	315
ATTACACCGTG CCACTCTGTT CGCCGTCAAA GTGCGCCCCG	355
TTATCCACGA TGGCCTCTTT TTCCGGCACA TGCTGCACGG	395

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CGGTGATGGC ATACGTGCCG TCGTCGTTCT CACGGATACT	435
CACGCAGCGG AACAGTCCTG GCGCAGCGTC GGCAGCTTCA	475
GCTCCCATAC GCTGTATTCA GCT	498

SEQ ID NO.: 4

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 685 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG TTG GAC GGG GTG CGG CTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AGA CCT CTC CTG CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Arg Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTC CAG GTC GGG CTC AAC CAA TAC CCG GTT GGG TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Tyr Pro Val Gly Ser	
30 35	
CCG CTC CCA TGT GAG CCC GAA CCG GAT GTA ACA GTG GTC	156
Pro Leu Pro Cys Glu Pro Glu Pro Asp Val Thr Val Val	
40 45 50	
ACT TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCG GAA	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
ACT GCC AGG CGT AGG TTG GCC AGG GGG AGT CCC CCT TCC	234
Thr Ala Arg Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCA GCT AGT CAG TTG TCT GCA CCT TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGT ACT ACC CAT CAT GAC TCT CCA GAC	312
Leu Lys Ala Thr Cys Thr Thr His His Asp Ser Pro Asp	
95 100	

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GCT	GAT	CTC	ATC	GAG	GCC	AAC	CTT	CTA	TGG	CGG	CAG	GAG	351
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	
105					110					115			
ATG	GGC	GGG	AAC	ATC	ACC	CGT	GTG	GAG	TCA	GAG	AAT	AAG	390
Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	
		120					125					130	
GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTT	CGA	GCG	GAG	429
Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	
				135						140			
GAG	GAT	GAG	AGG	GAA	GTA	TCC	GTT	GCG	GCG	GAG	ATC	CTG	468
Glu	Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	
	145					150					155		
CGG	AGA	ACC	AGG	AGA	TTC	CCC	CCG	GCG	ATA	CCT	GTA	TGG	507
Arg	Arg	Thr	Arg	Arg	Phe	Pro	Pro	Ala	Ile	Pro	Val	Trp	
			160					165					
GCG	CGC	CCG	GAC	TAC	AAC	CCG	CCA	CTG	ATA	GAA	TCT	TGG	546
Ala	Arg	Pro	Asp	Tyr	Asn	Pro	Pro	Leu	Ile	Glu	Ser	Trp	
170					175					180			
AAG	GAC	CCA	GAC	TAC	GTC	CCA	CCG	GTG	GTA	CAC	GGG	TGT	585
Lys	Asp	Pro	Asp	Tyr	Val	Pro	Pro	Val	Val	His	Gly	Cys	
		185					190					195	
CCA	TTG	CCA	CCT	GCC	AAG	ACC	CCT	CAA	GTG	GAT	ATT	CAG	624
Pro	Leu	Pro	Pro	Ala	Lys	Thr	Pro	Gln	Val	Asp	Ile	Gln	
				200					205				
ACC	TCT	TTG	AGG	CTT	TCG	TTG	GAA	ACG	GGA	TTT	CTT	CAT	663
Thr	Ser	Leu	Arg	Leu	Ser	Leu	Glu	Thr	Gly	Phe	Leu	His	
	210					215					220		
ACT	ATG	CTA	GAC	AGA	AGA	ATT	C						685
Thr	Met	Leu	Asp	Arg	Arg	Ile							
			225										

`SEQ ID NO.: 5

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 608 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

TG ATA GCG TTC GCT TCG CGG GGA AAC CAC GTC TCC CCC	38
Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro	
5 10	
ACG CAC TAT GTG CCT GAA AGC GAC GCT GCA GCG CGT GTC	77
Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val	
15 20 25	
ACC CAG ATC CTC TCC AGC CTT ACC ATC ACT CAG CTG TTG	116
Thr Gln Ile Leu Ser Ser Leu Thr Ile Thr Gln Leu Leu	
30 35	
AAG AGG CTC CAC CAG TGG ATC AAT GAG GAC TGC TCC ACG	155
Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser Thr	
40 45 50	
CCA TGC TCC GGT TCG TGG CTT AGG GAT GTT TGG GAC TGG	194
Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp	
55 60	
ATA TGC ACG GTG TTG ACT GAC TTC AAA ACC TGG CTC CAG	233
Ile Cys Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln	
65 70 75	
TCC AAG CTC CTG CCG CGA TTG CCG GGA GTC CCT TTC CTT	272
Ser Lys Leu Leu Pro Arg Leu Pro Gly Val Pro Phe Leu	
80 85 90	
TCA TGC CAA CGA GGG TAC AAG GGA GTC TGG CGG GGA GAT	311
Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp	
95 100	

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GGT	GTC	ATG	CAA	ACC	ACC	TGC	CCA	TGT	GGA	GCA	CAG	ATC	350
Gly	Val	Met	Gln	Thr	Thr	Cys	Pro	Cys	Gly	Ala	Gln	Ile	
	105					110					115		
AGT	GGG	CAT	GTC	AAA	AAT	GGC	TCC	ATG	AGG	ATC	GTT	GGG	389
Ser	Gly	His	Val	Lys	Asn	Gly	Ser	Met	Arg	Ile	Val	Gly	
			120					125					
CCT	AGA	ACC	TGT	AGC	AAC	ACG	TGG	CAC	GGA	ACG	TTC	CCT	428
Pro	Arg	Thr	Cys	Ser	Asn	Thr	Trp	His	Gly	Thr	Phe	Pro	
130					135						140		
ATC	AAC	GCG	TAC	ACC	ACA	GGC	CCC	TGC	ACA	CCC	TCC	CCG	467
Ile	Asn	Ala	Tyr	Thr	Thr	Gly	Pro	Cys	Thr	Pro	Ser	Pro	
		145					150					155	
GCG	CCC	AAC	TAC	TCT	AGG	GCG	TTG	TGG	CGG	GTG	GCT	GCT	506
Ala	Pro	Asn	Tyr	Ser	Arg	Ala	Leu	Trp	Arg	Val	Ala	Ala	
				160						165			
GAG	GAG	TAC	GTG	GAG	GTC	ACG	CGG	GTG	GGG	GAT	TTC	CAC	545
Glu	Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly	Asp	Phe	His	
	170					175					180		
TAC	GTG	ACG	GGC	ATG	ACC	ACT	GAC	AAC	GTA	AGA	TGC	CCA	584
Tyr	Val	Thr	Gly	Met	Thr	Thr	Asp	Asn	Val	Arg	Cys	Pro	
			185					190					
TGC	CAG	GTT	CCG	GCC	CCC	GAA	TTC						608
Cys	Gln	Val	Pro	Ala	Pro	Glu	Phe						
195					200								

SEQ ID NO.: 6

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 473 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG TTG GAT GGG GTG CGG TTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCT GCA AAG CCT CTC CTA CGG GAT GAG GTC	78
Tyr Ala Pro Ala Ala Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTT CAG GTC GGG CTC AAC CAA TTC CCG GTT GGG TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Phe Pro Val Gly Ser	
30 35	
CAG CTC CCA TGT GAG CCC GAA CCG GAT GTA ACA GTG ATC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Thr Val Ile	
40 45 50	
ACC TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCA GAG	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
GCG GCT GGG CGT AGG CTG GCC AGA GGG TCT CCC CCT TCC	234
Ala Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCG GCT AGT CAG TTG TCT GCG CCC TTC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Phe	
80 85 90	
CCT GTT GAA GGC CGA CAT GCA CTA CCC GTC ATG ACT CCC	312
Pro Val Glu Gly Arg His Ala Leu Pro Val Met Thr Pro	
95 100	

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CAG	ACG	CTG	ACC	TCA	TCG	AGG	CCA	ATC	TCC	TGT	GGC	GGC	351
Gln	Thr	Leu	Thr	Ser	Ser	Arg	Pro	Ile	Ser	Cys	Gly	Gly	
105					110					115			
AGG	AGA	TGG	GAG	GGA	ACA	TCA	CCC	GCG	TGG	AGT	CAG	AGA	390
Arg	Arg	Trp	Glu	Gly	Thr	Ser	Pro	Ala	Trp	Ser	Gln	Arg	
		120					125					130	
ACA	AGG	TAC	TAATCCTAGA	CTCTTTTGAC	CCGCTCCGAG								429
Thr	Arg	Tyr											
CGGAGGAGGA	TGAGAGGGAG	ATATCTGTTG	CGGCCAGCT	GAGC									473

SEQ ID NO.: 7

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 526 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG CTG GAT GGG GTG CGG TTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AAG CCT CTC CTA CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTT CAG GTC GGG CTC AAC CAA TTC CCG GTT GGG TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Phe Pro Val Gly Ser	
30 35	
CAG CTC CCG TGT GAG CCC GAA CCG GAT GTA ACG GTG ATC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Thr Val Ile	
40 45 50	
ACT TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCA GAG	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
ACG GCT GGG CGT AGG CTG GCC AGA GGG TCT CCC CCT TCC	234
Thr Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCG GCT AGT CAG TTG TCT GCG CCC TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCA ACA TGC ACT ACC CGT CAT GAC TCC CCA GAC	312
Leu Lys Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp	
95 100	

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GCT	GAC	CTC	ATC	GAG	GCC	AAT	CTC	CTG	TGG	CGG	CAG	GAG	351
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	
105					110					115			
ATG	GGA	GGG	AAC	ATC	ACC	CGC	GTG	GAG	TCA	GAG	AAC	AAG	390
Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	
		120					125					130	
GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTC	CGA	GCG	GAG	429
Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	
				135						140			
GAG	GAT	GAG	AGG	GAG	ATA	TCT	GTT	GCG	GCG	GAG	ATC	CTA	468
Glu	Asp	Glu	Arg	Glu	Ile	Ser	Val	Ala	Ala	Glu	Ile	Leu	
		145				150					155		
CGG	AAA	TCT	AGG	AAA	TTC	CCC	CCA	GCA	TTA	CCC	ATA	TGG	507
Arg	Lys	Ser	Arg	Lys	Phe	Pro	Pro	Ala	Leu	Pro	Ile	Trp	
			160					165					
GCG	CGC	CCG	GAC	TAC	AACC								526
Ala	Arg	Pro	Asp	Tyr	Asn								
170					175								

SEQ ID NO.: 8

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 599 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG TTG GAT GGG GTG CGG CTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AAA CCT CTC CTG CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACG TTC CAG GTC GGG CTC AAC CAA TAC CCG GTT GGA TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Tyr Pro Val Gly Ser	
30 35	
CAG CTC CCA TGC GAG CCC GAA CCG GAT GTG GCG GTG CTC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Ala Val Leu	
40 45 50	
ACT TCC ATG CTC ACC GAC CCC ACC CAC ATT ACA GCA GAA	195
Thr Ser Met Leu Thr Asp Pro Thr His Ile Thr Ala Glu	
55 60 65	
GCG GCT AGG CGC AGG CTG GCC AGA GGG TCT CCT CCT TCC	234
Ala Ala Arg Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCA GCT AGT CAG TTG TCT GCG CCC TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGC ACT ACC CAT CAT GAC TCC CCA GAC	312
Leu Lys Ala Thr Cys Thr Thr His His Asp Ser Pro Asp	
95 100	

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GCT	GAC	CTC	ATC	GAG	GCC	AAC	CTC	CTG	TGG	CGG	CAG	GAG	351
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	
105					110					115			
ATG	GGC	GGA	AAC	ATC	ACC	CGC	GTG	GAG	TCA	GAG	AAT	AAG	390
Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	
		120					125					130	
GTA	GTA	ATT	CTA	GAC	TCT	TTT	GAA	CCG	CTT	CGA	GCG	GAA	429
Val	Val	Ile	Leu	Asp	Ser	Phe	Glu	Pro	Leu	Arg	Ala	Glu	
				135					140				
GAG	GAT	GAG	AGG	GAA	GTA	TCC	GTT	GCG	GCA	GAG	ATC	CTG	468
Glu	Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	
	145					150					155		
CGG	AAA	ACC	AGG	AGA	TTC	CCC	GCA	GCG	ATG	CCC	ATA	TGG	507
Arg	Lys	Thr	Arg	Arg	Phe	Pro	Ala	Ala	Met	Pro	Ile	Trp	
			160					165					
GCA	CGT	CCG	GAC	TAC	AAC	CCA	CCA	TTA	CTA	CAG	TCC	TGG	546
Ala	Arg	Pro	Asp	Tyr	Asn	Pro	Pro	Leu	Leu	Gln	Ser	Trp	
170					175					180			
AAG	GAC	CCG	GAC	TAC	GTC	CCT	CCG	GTG	GTG	CAC	GGG	TGC	585
Lys	Asp	Pro	Asp	Tyr	Val	Pro	Pro	Val	Val	His	Gly	Cys	
		185					190					195	
CCA	TTG	CCA	CCT	GC									599
Pro	Leu	Pro	Pro										

SEQ ID NO.: 9

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 1184 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG TTG GAT GGG GTG CGG CTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AAA CCT CTC CTG CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACG TTC CAG GTC GGG CTC AAC CAA TAC CCG GTT GGA TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Tyr Pro Val Gly Ser	
30 35	
CAG CTC CCA TGC GAG CCC GAA CCG GAT GTG GCG GTG CTC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Ala Val Leu	
40 45 50	
ACT TCC ATG CTC ACC GAC CCC ACC CAC ATT ACA GCA GAA	195
Thr Ser Met Leu Thr Asp Pro Thr His Ile Thr Ala Glu	
55 60 65	
GCG GCT AGG CGC AGG CTG GCC AGA GGG TCT CCT CCT TCC	234
Ala Ala Arg Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCA GCT AGT CAG TTG TCT GCG CCC TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGC ACT ACC CAT CAT GAC TCC CCA GAC	312
Leu Lys Ala Thr Cys Thr Thr His His Asp Ser Pro Asp	
95 100	

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GCT Ala 105	GAC Asp	CTC Leu	ATC Ile	GAG Glu	GCC Ala 110	AAC Asn	CTC Leu	CTG Leu	TGG Trp	CGG Arg 115	CAG Gln	GAG Glu	351
ATG Met	GGC Gly	GGA Gly 120	AAC Asn	ATC Ile	ACC Thr	CGC Arg	GTG Val 125	GAG Glu	TCA Ser	GAG Glu	AAT Asn	AAG Lys 130	390
GTA Val	GTA Val	ATT Ile	CTA Leu	GAC Asp 135	TCT Ser	TTT Phe	GAA Glu	CCG Pro	CTT Leu	CGA Arg	GCG Ala	GAA Glu	429
GAG Glu	GAT Asp 145	GAG Glu	AGG Arg	GAA Glu	GTA Val	TCC Ser 150	GTT Val	GCG Ala	GCA Ala	GAG Glu	ATC Ile 155	CTG Leu	468
CGG Arg	AAA Lys	ACC Thr	AGG Arg 160	AGA Arg	TTC Phe	CCC Pro	GCA Ala	GCG Ala	ATG Met	CCC Pro	ATA Ile	TGG Trp	507
GCA Ala 170	CGT Arg	CCG Pro	GAC Asp	TAC Tyr	AAC Asn 175	CCA Pro	CCA Pro	TTA Leu	CTA Leu	CAG Gln	TCC Ser	TGG Trp	546
AAG Lys	GAC Asp	CCG Pro 185	GAC Asp	TAC Tyr	GTC Val	CCT Pro	CCG Pro 190	GTG Val	GTG Val	CAC His	GGG Gly	TGC Cys 195	585
CCA Pro	TTG Leu	CCA Pro	CCT Pro	GCC Ala 200	AAG Lys	GCC Ala	CCT Pro	CCA Pro	GTA Val 205	CCA Pro	CCT Pro	CCA Pro	624
AGG Arg	AGA Arg	AAG Lys	AGG Arg	ACG Thr	GTT Val 210	GTC Val 215	CTG Leu	ACA Thr	GAA Glu	TCC Ser	ACC Thr	GTG Val 220	663
TCT Ser	TCC Ser	GCC Ala	TTG Leu 225	GCG Ala	GAG Glu	CTT Leu	GCT Ala	ACA Thr 230	AAG Lys	ACC Thr	TTC Phe	GGC Gly	702
GGG Gly 235	TCC Ser	GGA Gly	TCA Ser	TCG Ser	GCC Ala 240	GCC Ala	GAC Asp	AGC Ser	GGC Gly	ACA Thr 245	GCA Ala	AGC Ser	741
GGC Gly	CCT Pro	CCT Pro 250	GGC Gly	CAG Gln	GCC Ala	TCC Ser	GAC Asp 255	GAT Asp	GGA Gly	GAT Asp	ACA Thr	GGA Gly 260	780
TCC Ser	GAC Asp	GTT Val	GAG Glu	TCG Ser 265	TAC Tyr	TCC Ser	TCC Ser	ATG Met	CCC Pro 270	CCC Pro	CTT Leu	GAG Glu	819

GGA	GAG	CCG	GGG	GAC	CCC	GAC	CTC	AGC	GAC	GGG	TCT	TGG	858
Gly	Glu	Pro	Gly	Asp	Pro	Asp	Leu	Ser	Asp	Gly	Ser	Trp	
	275					280					285		
TCT	ACT	GTG	AGT	GAG	GAG	GCT	GGT	GAG	GAT	GTC	GTC	TGC	897
Ser	Thr	Val	Ser	Glu	Glu	Ala	Gly	Glu	Asp	Val	Val	Cys	
			290					295					
TGC	TCG	ATG	TCC	TAC	ACA	TGG	ACA	GGC	GCC	TTA	ATC	ACA	936
Cys	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Gly	Ala	Leu	Ile	Thr	
300					305					310			
CCA	TGC	ACC	GCG	GAG	GAG	AGC	AAG	CTG	CCC	ATC	AAC	CCG	975
Pro	Cys	Thr	Ala	Glu	Glu	Ser	Lys	Leu	Pro	Ile	Asn	Pro	
		315					320					325	
TTG	AGC	AAC	TCT	TTG	CTG	CGG	GCA	TCT	GCT	CGG	GCG	TAT	1014
Leu	Ser	Asn	Ser	Leu	Leu	Arg	Ala	Ser	Ala	Arg	Ala	Tyr	
				330					335				
CAT	CAA	CTG	ATG	AGC	AAG	AAG	GAT	ATA	ATT	CCT	ACG	CCC	1053
His	Gln	Leu	Met	Ser	Lys	Lys	Asp	Ile	Ile	Pro	Thr	Pro	
	340					345					350		
TCT	CAG	CCG	ATG	AAC	AGT	TGG	AAT	AGG	TTG	TTA	GCG	GTA	1092
Ser	Gln	Pro	Met	Asn	Ser	Trp	Asn	Arg	Leu	Leu	Ala	Val	
			355					360					
ACT	AAG	ATT	AGT	ATG	GTA	ATT	AGG	AAA	ATG	AGT	AGA	TAT	1131
Thr	Lys	Ile	Ser	Met	Val	Ile	Arg	Lys	Met	Ser	Arg	Tyr	
365					370					375			
TTG	AAG	AAC	TTGATTAATGT	TTGGGTCTGA	GTTTATATAT								1170
Leu	Lys	Asn											
		380											
CACAGTGAGA	ATTC												1184

SEQ ID NO.: 10

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 255 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GGG CAT GTC AAA AAT GGC TCC ATG AGG ATC GTT GGG CCT	39
Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro	
5 10	
AGA ACC TGT AGC AAC ACG TGG CAC GGA ACG TTC CCT ATC	78
Arg Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile	
15 20 25	
AAC GCG TAC ACC ACA GGC CCC TGC ACA CCC TCC CCG GCG	117
Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala	
30 35	
CCC AAC TAC TCT AGG GCG TTG TGG CGG GTG GCT GCT GAG	156
Pro Asn Tyr Ser Arg Ala Leu Trp Arg Val Ala Ala Glu	
40 45 50	
GAG TAC GTG GAG GTC ACG CGG GTG GGG GAT TTC CAC TAC	195
Glu Tyr Val Glu Val Thr Arg Val Gly Asp Phe His Tyr	
55 60 65	
GTG ACG GGC ATG ACC ACT GAC AAC GTA AGA TGC CCA TGC	234
Val Thr Gly Met Thr Thr Asp Asn Val Arg Cys Pro Cys	
70 75	
CAG GTT CCG GCC CCC GAA TTC	255
Gln Val Pro Ala Pro Glu Phe	
80 85	

SEQ ID NO.: 11

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 553 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG TTG GAT GGG GTG CGG TTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AAA CCT CTC CTA CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTT CAG GTC GGG CTC AAC CAA TTC CCG GTT GGG TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Phe Pro Val Gly Ser	
30 35	
CAG CTC CCA TGT GAG CCC GAA CCG GAT GTA ACA GTG ATC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Thr Val Ile	
40 45 50	
ACC TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCA GAG	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
ACG GCT GGG CGT AGG CTG GCC AGA GGG TCT CCC CCT TCC	234
Thr Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCG GCT AGT CAG TTG TCT GCG CCT TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGC ACT ACC CGT CAT GAC TCC CCA GAC	312
Leu Lys Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp	
95 100	

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GCT	GAC	CTC	ATC	GAG	GCC	AAT	CTC	CTG	TGG	CGG	CAG	GAG	351
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	
105					110					115			
ATG	GGA	GGG	AAC	ATC	ACC	CGC	GTG	GAG	TCA	GAG	AAC	AAG	390
Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	
		120					125					130	
GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTC	CGA	GCG	GAG	429
Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	
				135					140				
GAG	GAT	GAG	AGG	GAG	ATA	TCT	GTT	GCG	GCG	GAG	ATC	CTA	468
Glu	Asp	Glu	Arg	Glu	Ile	Ser	Val	Ala	Ala	Glu	Ile	Leu	
	145					150					155		
CGG	AAA	TCT	AGG	AAA	TTC	CCC	CCA	GCA	TTA	CCC	ATA	TGG	507
Arg	Lys	Ser	Arg	Lys	Phe	Pro	Pro	Ala	Leu	Pro	Ile	Trp	
			160					165					
GCG	CGC	CCG	GAC	TAC	AAC	CCA	CCA	CTG	CTA	GAG	TCT	TGG	546
Ala	Arg	Pro	Asp	Tyr	Asn	Pro	Pro	Leu	Leu	Glu	Ser	Trp	
170					175					180			
CCA	GCT	G											553
Pro	Ala												

SEQ ID NO.: 12

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 884 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

CG GCT TTC GTG GGC GCC GGC ATA GCC GGC GCG GCT GTT	38
Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Val	
5 10	
GGC AGC ATA GGC CTT GGG AAG GTG CTT GTG GAC ATC CTG	77
Gly Ser Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu	
15 20 25	
GCG GGT TAT GGA GCA GGG GTG GCA GGC GCA CTC GTG GTC	116
Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu Val Val	
30 35	
TTT AAG GTT ATG AGT GGC GAC ATG CCC TCC ACC GAG GAC	155
Phe Lys Val Met Ser Gly Asp Met Pro Ser Thr Glu Asp	
40 45 50	
CTG GTC AAC TTA CTC CCT GCC ATC CTT TCC CCT GGC GCC	194
Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala	
55 60	
CTG GTC GTC GGG GTC GTG TGC GCA CAG ATA CTG CGT CGA	233
Leu Val Val Gly Val Val Cys Ala Gln Ile Leu Arg Arg	
65 70 75	
CAT GTC GGC CCA GGG GAG GGA GCT GTG CAG TGG ATG AAC	272
His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn	
80 85 90	
CGG CTG ATA GCG TTC GCT TCG CGG GGT AAC CAC GTC TCC	311
Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser	
95 100	

CCC	ACG	CAT	TAT	GTG	CCT	GAA	AGC	GAC	GCT	GCG	AGT	CGT	350
Pro	Thr	His	Tyr	Val	Pro	Glu	Ser	Asp	Ala	Ala	Ser	Arg	
	105					110					115		
GTC	ACC	CAG	ATC	CTC	TCC	AGC	CTT	ACC	ATC	ACT	CAG	CTG	389
Val	Thr	Gln	Ile	Leu	Ser	Ser	Leu	Thr	Ile	Thr	Gln	Leu	
			120					125					
TTG	AAG	AGG	CTC	CAC	CAG	TGG	ATT	AAT	GAG	GAC	TGC	TCC	428
Leu	Lys	Arg	Leu	His	Gln	Trp	Ile	Asn	Glu	Asp	Cys	Ser	
130					135					140			
ACG	CCA	TGC	TCC	GGC	ACG	TGG	CTC	AGG	GAT	GTT	TGG	GAC	467
Thr	Pro	Cys	Ser	Gly	Thr	Trp	Leu	Arg	Asp	Val	Trp	Asp	
		145					150					155	
TGG	ATA	TGC	ACG	GTG	TTG	GCT	GAC	TTC	AAG	ACC	TGG	CTC	506
Trp	Ile	Cys	Thr	Val	Leu	Ala	Asp	Phe	Lys	Thr	Trp	Leu	
				160					165				
CAG	TCC	AAG	CTC	CTG	CCG	CGG	TTA	CCG	GGG	GTC	CCT	TTC	545
Gln	Ser	Lys	Leu	Leu	Pro	Arg	Leu	Pro	Gly	Val	Pro	Phe	
	170					175					180		
CTC	TCA	TGT	CAG	CGT	GGG	TAC	AAG	GGA	GTT	TGG	CGG	GGA	584
Leu	Ser	Cys	Gln	Arg	Gly	Tyr	Lys	Gly	Val	Trp	Arg	Gly	
			185					190					
GAT	GGC	ATC	ATG	CAC	ACC	ACC	TGC	CCA	TGC	GGA	GCC	CAA	623
Asp	Gly	Ile	Met	His	Thr	Thr	Cys	Pro	Cys	Gly	Ala	Gln	
195					200					205			
ATC	ACC	GGA	CAT	GTC	AAA	AAC	GGG	TCC	ATG	AGG	ATC	GCC	662
Ile	Thr	Gly	His	Val	Lys	Asn	Gly	Ser	Met	Arg	Ile	Ala	
		210					215					220	
GGG	CCT	AAA	ACC	TGC	AGC	AAC	ACG	TGG	CAC	GGA	ACG	TTC	701
Gly	Pro	Lys	Thr	Cys	Ser	Asn	Thr	Trp	His	Gly	Thr	Phe	
				225					230				
CCC	ATT	AAC	GCA	TAC	ACC	ACA	GGC	CCC	TGC	ACA	CCC	TCT	740
Pro	Ile	Asn	Ala	Tyr	Thr	Thr	Gly	Pro	Cys	Thr	Pro	Ser	
	235					240					245		
CCG	GCG	CCA	AAC	TAC	TCC	AGG	GCG	TTG	TGG	CGG	GTG	GCT	779
Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala	Leu	Trp	Arg	Val	Ala	
			250					255					
GCG	GAG	GAG	TAC	GTG	GAG	GTC	ACG	CGG	GTG	GGG	GAT	TTC	818
Ala	Glu	Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly	Asp	Phe	
260					265					270			

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CAC	TAC	GTG	ACG	GGC	ATG	ACC	ACT	GAC	AAT	GTA	AAA	TGC	857
His	Tyr	Val	Thr	Gly	Met	Thr	Thr	Asp	Asn	Val	Lys	Cys	
		275					280					285	
CCA	TGC	CAG	GTT	CCG	GCC	CCC	GAA	TTC					884
Pro	Cys	Gln	Val	Pro	Ala	Pro	Glu	Phe					
				290									

SEQ ID NO.: 13

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 524 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACA GAG TTG GAC GGG GTG CGG CTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AGA CCT CTC CTG CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Arg Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTC CAG GTC GGG CTC AAC CAA TAC CCG GTT GGG TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Tyr Pro Val Gly Ser	
30 35	
CAG CTC CCA TGT GAG CCC GAA CCG GAT GTA ACA GTG GTC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Thr Val Val	
40 45 50	
ACT TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCG GAA	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
ACT GCC AGG CGT AGG TTG GCC AGG GGG AGT CCC CCT TCC	234
Thr Ala Arg Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCA GCT AGT CAG TTG TCT GCA CCT TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGT ACT ACC CAT CAT GAC TCT CCA GAC	312
Leu Lys Ala Thr Cys Thr Thr His His Asp Ser Pro Asp	
95 100	

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GCT	GAT	CTC	ATC	GAG	GCC	AAC	CTT	CTA	TGG	CGG	CAG	GAG	351
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	
105					110					115			
ATG	GGC	GGG	AAC	ATC	ACC	CGT	GTG	GAG	TCA	GAG	AAT	AAG	390
Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	
		120					125					130	
GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTT	CGA	GCG	GAG	429
Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	
				135					140				
GAG	GAT	GAG	AGG	GAA	GTA	TCC	GTT	GCG	GCG	GAG	ATC	CTG	468
Glu	Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	
	145					150					155		
CGG	AGA	ACC	AGG	AGA	TTC	CCC	CCG	GCG	ATA	CCT	GTA	TGG	507
Arg	Arg	Thr	Arg	Arg	Phe	Pro	Pro	Ala	Ile	Pro	Val	Trp	
			160					165					
GCG	CGC	CCG	GAC	CAG	CT								524
Ala	Arg	Pro	Asp	Gln									
170													

SEQ ID NO.: 14

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 174 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC AGC AAA GTT TCC AGA TAC AAG ATT AAT GGA CAC	39
Glu Phe Ser Lys Val Ser Arg Tyr Lys Ile Asn Gly His	
5 10	
AAA TCA GTA GCT CTT CCA TAC ATC AAC AGC TAC CAA GCA	78
Lys Ser Val Ala Leu Pro Tyr Ile Asn Ser Tyr Gln Ala	
15 20 25	
GAG AAT CAC ATC AAG AAC TCA ACC CCT TTT ACA ATA GCT	117
Glu Asn His Ile Lys Asn Ser Thr Pro Phe Thr Ile Ala	
30 35	
GCG ACA AAC AAC AAC AAC AAA AAA ACA AAA CTT AGG AAT	156
Ala Thr Asn Asn Asn Asn Lys Lys Thr Lys Leu Arg Asn	
40 45 50	
ATA CCT AGC AAA GAA TTC	174
Ile Pro Ser Lys Glu Phe	
55	

SEQ ID NO.: 15

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 135 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA	TTC	CCT	AGC	CTG	GGC	AAC	AGA	GTG	AGA	GTC	CGT	CTC	39
Glu	Phe	Pro	Ser	Leu	Gly	Asn	Arg	Val	Arg	Val	Arg	Leu	
				5						10			
AAA	AAA	AAA	AAA	ACA	ACA	ACA	AAA	AAA	ACA	AAC	CCA	CAA	78
Lys	Lys	Lys	Lys	Thr	Thr	Thr	Lys	Lys	Thr	Asn	Pro	Gln	
	15					20					25		
AAC	TGC	AGC	CAC	CTA	TGT	CCC	TAC	CTC	CCC	AGC	CTC	CAG	117
Asn	Cys	Ser	His	Leu	Cys	Pro	Tyr	Leu	Pro	Ser	Leu	Gln	
			30					35					
GGC	CCC	TTC	CGG	AAT	TCC								135
Gly	Pro	Phe	Arg	Asn	Ser								
40					45								

SEQ ID NO.: 16

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 306 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC GCG GGA ACC CGG GAG GCG GAC GTT GCA GTG AGC	39
Glu Phe Ala Gly Thr Arg Glu Ala Asp Val Ala Val Ser	
5 10	
CGA GAT CGC GCC ACT GCA CTC CAG CCT GGG CGA CAG AGC	78
Arg Asp Arg Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser	
15 20 25	
AAG ACT CTG TCT CAA AAA AAA AAA AAC AAA AAC AAA AAG	117
Lys Thr Leu Ser Gln Lys Lys Lys Asn Lys Asn Lys Lys	
30 35	
AAG GAC TGG GAG GGT CGG CAG TAATCGAGGA CCACCTGGCA	158
Lys Asp Trp Glu Gly Arg Gln	
40 45	
GTGACAGAGG GTGACCCAGG GCTGGGAGGA TACCCAGGG	198
GAGACCCAG GCTCTGAAAA GTGCCTTGCC ATTCAATCTA	238
CTTCAGTAAT AGCATGTGTC ATGGGATAGA TAATAAAATC	278
CGGAGGGGAA AAAATGCTCG CGGAATTC	306

SEQ ID NO.: 17

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 174 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC AGC ACA GTT TCC AGA TAC AAG ATT AAT GGA CAC	39
Glu Phe Ser Thr Val Ser Arg Tyr Lys Ile Asn Gly His	
5 10	
AAA TCA GTA GCT CTT CCA TAC ATC AAC AGC TAC CAA GCA	78
Lys Ser Val Ala Leu Pro Tyr Ile Asn Ser Tyr Gln Ala	
15 20 25	
GAG AAT CAC ATC AAG AAC TCA ACC CCT TTT ACA ATA GCT	117
Glu Asn His Ile Lys Asn Ser Thr Pro Phe Thr Ile Ala	
30 35	
GCG ACA AAC AAC AAC AAC AAA AAA ACA AAA CTT AGG AAT	156
Ala Thr Asn Asn Asn Asn Lys Lys Thr Lys Leu Arg Asn	
40 45 50	
ATA CCT AGC AAA GAA TTC	174
Ile Pro Ser Lys Glu Phe	
55	

SEQ ID NO.: 18

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 95 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC CCT AAA AAA GAA AAA AAA AAA AAA AGA CTT CAG	39
Glu Phe Pro Lys Lys Glu Lys Lys Lys Lys Arg Leu Gln	
5 10	
CCA ACA GAT CAG AAC GCA GAA AAT GCA TTT GCC TCA GTA	78
Pro Thr Asp Gln Asn Ala Glu Asn Ala Phe Ala Ser Val	
15 20 25	
GTG AGT CGG CAG AAT TC	95
Val Ser Arg Gln Asn	
30	

SEQ ID NO.: 19

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 668 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACG GAA TTG GAT GGG GTG CGG CTA CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AAG CCT CTC CTA CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTC CAG GTC GGG CTC AAC CAA TTC CCG GTT GGG TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Phe Pro Val Gly Ser	
30 35	
CAG CTC CCA TGT GAA CCC GAA CCG GAT GTA ATG GTG GTC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Met Val Val	
40 45 50	
ACC TCT ATG CTC ACC GAC CCC TCC CAT ATT ACA GCA GAG	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
ACG GCT AAG CGT AGG CTG GCC AGA GGG TCT CCC CCT TCT	234
Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCA GCT AGT CAG TTG TCT GCG CCC TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGC ACC ACC CGT CAT GAC TCC CCG GAC	312
Leu Lys Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp	
95 100	

GCT GAC CTC ATA GAG GCC AAC CTC CTG TGG CGG CAG GAG	351
Ala Asp Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu	
105 110 115	
ATG GGC GGG AAC ATC ACC CGT GTG GAG TCA GAG AAT AAG	390
Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu Asn Lys	
120 125 130	
GTA GTG ATT TTG GAC TCT TTT GAA CCG CTT CGG GTG GAG	429
Val Val Ile Leu Asp Ser Phe Glu Pro Leu Arg Val Glu	
135 140	
GAG GAT GAG AGG GAA GTA TCC GTA GCG GCG GAT TTC AGT	468
Glu Asp Glu Arg Glu Val Ser Val Ala Ala Asp Phe Ser	
145 150 155	
GAC TTG AAT GCA GAA TGAATCCCGT GGCTCACTTC	503
Asp Leu Asn Ala Glu	
160	
CTAGACTATT TGCCAAAGAA GATGTTGCCC TGGCCATGAT	543
CAAGATGACA CAAACGGTGG CCTTTTGCAG GGAGAACCGC	583
CGTGGAGGCC TGTGTCTGTG GCACTGGTAG CTTCTCTCTG	623
CAGGCAAAGA CCCCATGGCT TAGTTCTTCA TCAGAGTGAG AATTC	668

SEQ ID NO.: 20

SEQUENCE TYPE: Nucleotide with corresponding peptide

SEQUENCE LENGTH: 479 base pairs

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

PROPERTIES: blood-borne non-A, non-B hepatitis specific
antigenic protein coding gene

GAA TTC TTC ACG GAG TTG GAT GGG GTA CGG CTG CAC AGG	39
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg	
5 10	
TAC GCT CCG GCG TGC AAG CCA CTC CTA CGG GAT GAG GTC	78
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Asp Glu Val	
15 20 25	
ACA TTC CAG GTC GGG CTC AAC CAA TTT CCA GTT GGA TCA	117
Thr Phe Gln Val Gly Leu Asn Gln Phe Pro Val Gly Ser	
30 35	
CAG CTC CCA TGT GAG CCC GAG CCG GAT GTA GCG GTG CTC	156
Gln Leu Pro Cys Glu Pro Glu Pro Asp Val Ala Val Leu	
40 45 50	
ACT TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCA GAG	195
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu	
55 60 65	
ACG GCT AAG CGT AGG CTG GCC AGG GGG TCC CCC CCC TCC	234
Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser	
70 75	
TTG GCC AGC TCT TCA GCT AGT CAG TTG TCT GCG CCC TCC	273
Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser	
80 85 90	
TTG AAG GCG ACA TGC ACT ACC CAC CAT GAC TCC CCG GAC	312
Leu Lys Ala Thr Cys Thr Thr His His Asp Ser Pro Asp	
95 100	

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GCT	GAC	CTC	ATC	GAG	GCC	AAC	CTC	CTG	TGG	CGG	CAG	GAG	351
Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	
105					110					115			
ATG	GGA	GGA	AAC	ATC	ACC	CGC	GTG	GAG	TCA	GAG	AAT	AAG	390
Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn	Lys	
		120					125					130	
GTA	GTA	ATT	CTA	GAC	TCT	TTT	GAC	CCG	CTC	CGA	GCG	GAG	429
Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	
				135					140				
GAG	GAT	GAG	AGG	GAA	GTG	TCC	GTT	GCG	GCG	GAG	ATC	CTG	468
Glu	Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	
	145					150					155		
CGG	AAG	ACC	AG										479
Arg	Lys	Thr											

Fig.1

10	20	30	40	50	60
GAATTCTTCA	CGGAATTGGA	TGGGGTGCGG	CTACACAGGT	ACGCTCCGGC	GTGCAAGCCT
70	80	90	100	110	120
CTCCTACGGG	ATGAGGTCAC	ATTCCAGGTC	GGGCTCAACC	AATTCCCAGT	TGGGTCACAG
130	140	150	160	170	180
CTCCCATGTG	AACCCGAACC	GGATGTAATG	GTGGTCACCT	CTATGCTCAC	CGACCCCTCC
190	200	210	220	230	240
CATATTACAG	CAGAGACGGC	TAAGCGTAGG	CTGGCCAGAG	GGTCTCCCCC	TTCTTTGGCC
250	260	270	280	290	300
AGCTCTTCAG	CTAGTCAGTT	GTCTGCGCCC	TCCTTGAAGG	CGACATGCAC	CACCCGTCAT
310	320	330	340	350	360
GACTCCCCGG	ACGCTGACCT	CATAGAGGCC	AACCTCCTGT	GGCGGCAGGA	GATGGGCGGG
370	380	390	400	410	420
AACATCACCC	GTGTGGAGTC	AGAGAATAAG	GTAGTGATTT	TGGAATCTTT	TGAACCGCTT
430	440	450	460	470	480
CGGGTGGAGG	AGGATGAGAG	GGAAGTATCC	GTAGCGGCGG	ATTTCACTGA	CTTGAATGCA
490	500	510	520	530	540
GAATGAATCC	CGTGGCTCAC	TTCCTAGACT	ATTTGCCAAA	GAAGATGTTG	CCCTGGCCAT
550	560	570	580	590	600
GATCAAGATG	ACACAAACGG	TGGCCTTTTG	CAGGGAGAAC	CGCCGTGGAG	GCCTGTGTCT
610	620	630	640	650	660
GTGGCACTGG	TAGCTTCTCT	CTGCAGGCAA	AGACCCCATG	GCTTAGTTCT	TCATCAGAGT
670					
GAGAATTC					

Fig.2

10	20	30	40	50	60
GAATTC	TTCA	CGGAGTTGGA	TGGGGTACGG	CTGCACAGGT	ACGCTCCGGC
70	80	90	100	110	120
CTCCTACGGG	ATGAGGTCAC	ATTCCAGGTC	GGGCTCAACC	AATTTCCAGT	TGGATCACAG
130	140	150	160	170	180
CTCCCATGTG	AGCCCGAGCC	GGATGTAGCG	GTGCTCACTT	CCATGCTCAC	CGACCCCTCC
190	200	210	220	230	240
CACATTACAG	CAGAGACGGC	TAAGCGTAGG	CTGGCCAGGG	GGTCCCCCCC	CTCCTTGGCC
250	260	270	280	290	300
AGCTCTTCAG	CTAGTCAGTT	GTCTGCGCCC	TCCTTGAAGG	CGACATGCAC	TACCCACCAT
310	320	330	340	350	360
GACTCCCCGG	ACGCTGACCT	CATCGAGGCC	AACCTCCTGT	GGCGGCAGGA	GATGGGAGGA
370	380	390	400	410	420
AACATCACCC	GCGTGGAGTC	AGAGAATAAG	GTAGTAATTC	TAGACTCTTT	TGACCCGCTC
430	440	450	460	470	480
CGAGCGGAGG	AGGATGAGAG	GGAAGTGTCC	GTTGCGGCGG	AGATCCTGCG	GAAGACCAG

Fig.3

			10				20				30				40				
TCA	CTC	AAT	CCT	CGA	CGG	TGC	TGC	CGG	TGC	GGC	AAT	CCG	GAA	CGA	TAC				
Ser	Leu	Asn	Pro	Arg	Arg	Cys	Cys	Arg	Cys	Gly	Asn	Pro	Glu	Arg	Tyr				
			50				60				70				80				90
CGA	CGC	CGG	ATC	GCC	CTG	CTG	CCC	CCA	CGC	ATT	TAC	CGC	CCG	GAC	TGT				
Arg	Arg	Arg	Ile	Ala	Leu	Leu	Pro	Pro	Arg	Ile	Tyr	Arg	Pro	Asp	Cys				
			100				110				120				130				140
CAG	CCT	GTA	GTT	CCC	CAG	CGC	CAG	TTG	CGT	GAA	GCG	GTA	TGT	GGT	TTC				
Gln	Pro	Val	Val	Pro	Gln	Arg	Gln	Leu	Arg	Glu	Ala	Val	Cys	Gly	Phe				
			150				160				170				180				190
CGT	CGT	CCG	GGC	CGT	GCT	GAC	CAG	CCG	CTC	ACT	GCC	GTC	GTC	CGT	GTT				
Arg	Arg	Pro	Gly	Arg	Ala	Asp	Gln	Pro	Leu	Thr	Ala	Val	Val	Arg	Val				
			200				210				220				230				240
ACG	GTC	AGA	CGG	AGC	AGG	AAA	CTC	ACG	CCT	TCA	CAC	TTC	GGT	GTG	TCC				
Thr	Val	Arg	Arg	Ser	Arg	Lys	Leu	Thr	Pro	Ser	His	Phe	Gly	Val	Ser				
			250				260				270				280				290
CAT	CGC	GCC	AGC	ACC	TGATATTCCC	CGCTGTCTGC	AGTGACTTCT	GCGGTCAGGT											
His	Arg	Ala	Ser	Thr															
			300				310				320				330				340
GCTGCACCGC	TCGTGACACC	ATTCACCGTG	CCACTCTGTT	CGCCGTCAAA															
			350				360				370				380				390
GTGCGCCCCG	TTATCCACGA	TGGCCTCTTT	TTCCGGCACA	TGCTGCACGG															
			400				410				420				430				440
CGGTGATGGC	ATACGTGCCG	TCGTGCTTCT	CACGGATACTC	ACGCAGCGG															
			450				460				470				480				490
AACAGTCCTG	GCGCAGCGTC	GGCAGCTTCA	GCTCCCATAC	GCTGTATTCA	GCT														

Fig.4(1)

	10		20		30		40								
GAA	TTC	TTC	ACA	GAG	TTG	GAC	GGG	GTG	CGG	CTG	CAC	AGG	TAC	GCT	CCG
Glu	Phe	Phe	Thr	Glu	Leu	Asp	Gly	Val	Arg	Leu	His	Arg	Tyr	Ala	Pro
50		60		70		80		90							
GCG	TGC	AGA	CCT	CTC	CTG	CGG	GAT	GAG	GTC	ACA	TTC	CAG	GTC	GGG	CTC
Ala	Cys	Arg	Pro	Leu	Leu	Arg	Asp	Glu	Val	Thr	Phe	Gln	Val	Gly	Leu
100		110		120		130		140							
AAC	CAA	TAC	CCG	GTT	GGG	TCA	CCG	CTC	CCA	TGT	GAG	CCC	GAA	CCG	GAT
Asn	Gln	Tyr	Pro	Val	Gly	Ser	Pro	Leu	Pro	Cys	Glu	Pro	Glu	Pro	Asp
150		160		170		180		190							
GTA	ACA	GTG	GTC	ACT	TCC	ATG	CTC	ACC	GAC	CCC	TCC	CAC	ATT	ACA	GCG
Val	Thr	Val	Val	Thr	Ser	Met	Leu	Thr	Asp	Pro	Ser	His	Ile	Thr	Ala
200		210		220		230		240							
GAA	ACT	GCC	AGG	CGT	AGG	TTG	GCC	AGG	GGG	AGT	CCC	CCT	TCC	TTG	GCC
Glu	Thr	Ala	Arg	Arg	Arg	Leu	Ala	Arg	Gly	Ser	Pro	Pro	Ser	Leu	Ala
250		260		270		280									
AGC	TCT	TCA	GCT	AGT	CAG	TTG	TCT	GCA	CCT	TCC	TTG	AAG	GCG	ACA	TGT
Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	Lys	Ala	Thr	Cys
290		300		310		320		330							
ACT	ACC	CAT	CAT	GAC	TCT	CCA	GAC	GCT	GAT	CTC	ATC	GAG	GCC	AAC	CTT
Thr	Thr	His	His	Asp	Ser	Pro	Asp	Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu
340		350		360		370		380							
CTA	TGG	CGG	CAG	GAG	ATG	GGC	GGG	AAC	ATC	ACC	CGT	GTG	GAG	TCA	GAG
Leu	Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu
390		400		410		420		430							
AAT	AAG	GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTT	CGA	GCG	GAG	GAG
Asn	Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	Glu
440		450		460		470		480							
GAT	GAG	AGG	GAA	GTA	TCC	GTT	GCG	GCG	GAG	ATC	CTG	CGG	AGA	ACC	AGG
Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	Arg	Arg	Thr	Arg
490		500		510		520									
AGA	TTC	CCC	CCG	GCG	ATA	CCT	GTA	TGG	GCG	CGC	CCG	GAC	TAC	AAC	CCG
Arg	Phe	Pro	Pro	Ala	Ile	Pro	Val	Trp	Ala	Arg	Pro	Asp	Tyr	Asn	Pro
530		540		550		560		570							
CCA	CTG	ATA	GAA	TCT	TGG	AAG	GAC	CCA	GAC	TAC	GTC	CCA	CCG	GTG	GTA
Pro	Leu	Ile	Glu	Ser	Trp	Lys	Asp	Pro	Asp	Tyr	Val	Pro	Pro	Val	Val
580		590		600		610		620							
CAC	GGG	TGT	CCA	TTG	CCA	CCT	GCC	AAG	ACC	CCT	CAA	GTG	GAT	ATT	CAG
His	Gly	Cys	Pro	Leu	Pro	Pro	Ala	Lys	Thr	Pro	Gln	Val	Asp	Ile	Gln
630		640		650		660		670							
ACC	TCT	TTG	AGG	CTT	TCG	TTG	GAA	ACG	GGA	TTT	CTT	CAT	ACT	ATG	CTA
Thr	Ser	Leu	Arg	Leu	Ser	Leu	Glu	Thr	Gly	Phe	Leu	His	Thr	Met	Leu

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Fig.4(2)

680
GAC AGA AGA ATT C
Asp Arg Arg Ile

Fig.5

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      10      20      30      40
TG ATA GCG TTC GCT TCG CGG GGA AAC CAC GTC TCC CCC ACG CAC TAT
  Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr

      50      60      70      80      90
GTG CCT GAA AGC GAC GCT GCA GCG CGT GTC ACC CAG ATC CTC TCC AGC
Val Pro Glu Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser

     100     110     120     130     140
CTT ACC ATC ACT CAG CTG TTG AAG AGG CTC CAC CAG TGG ATC AAT GAG
Leu Thr Ile Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu

     150     160     170     180     190
GAC TGC TCC ACG CCA TGC TCC GGT TCG TGG CTT AGG GAT GTT TGG GAC
Asp Cys Ser Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp

     200     210     220     230
TGG ATA TGC ACG GTG TTG ACT GAC TTC AAA ACC TGG CTC CAG TCC AAG
Trp Ile Cys Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys

     240     250     260     270     280
CTC CTG CCG CGA TTG CCG GGA GTC CCT TTC CTT TCA TGC CAA CGA GGG
Leu Leu Pro Arg Leu Pro Gly Val Pro Phe Leu Ser Cys Gln Arg Gly

     290     300     310     320     330
TAC AAG GGA GTC TGG CGG GGA GAT GGT GTC ATG CAA ACC ACC TGC CCA
Tyr Lys Gly Val Trp Arg Gly Asp Gly Val Met Gln Thr Thr Cys Pro

     340     350     360     370     380
TGT GGA GCA CAG ATC AGT GGG CAT GTC AAA AAT GGC TCC ATG AGG ATC
Cys Gly Ala Gln Ile Ser Gly His Val Lys Asn Gly Ser Met Arg Ile

     390     400     410     420     430
GTT GGG CCT AGA ACC TGT AGC AAC ACG TGG CAC GGA ACG TTC CCT ATC
Val Gly Pro Arg Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile

     440     450     460     470
AAC GCG TAC ACC ACA GGC CCC TGC ACA CCC TCC CCG GCG CCC AAC TAC
Asn Ala Tyr Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr

     480     490     500     510     520
TCT AGG GCG TTG TGG CGG GTG GCT GCT GAG GAG TAC GTG GAG GTC ACG
Ser Arg Ala Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr

     530     540     550     560     570
CGG GTG GGG GAT TTC CAC TAC GTG ACG GGC ATG ACC ACT GAC AAC GTA
Arg Val Gly Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val

     580     590     600
AGA TGC CCA TGC CAG GTT CCG GCC CCC GAA TTC
Arg Cys Pro Cys Gln Val Pro Ala Pro Glu Phe

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Fig.7

	10	20	30	40											
GAA	TTC	TTC	ACA	GAG	CTG	GAT	GGG	GTG	CGG	TTG	CAC	AGG	TAC	GCT	CCG
Glu	Phe	Phe	Thr	Glu	Leu	Asp	Gly	Val	Arg	Leu	His	Arg	Tyr	Ala	Pro
50	60	70	80	90											
GCG	TGC	AAG	CCT	CTC	CTA	CGG	GAT	GAG	GTC	ACA	TTT	CAG	GTC	GGG	CTC
Ala	Cys	Lys	Pro	Leu	Leu	Arg	Asp	Glu	Val	Thr	Phe	Gln	Val	Gly	Leu
100	110	120	130	140											
AAC	CAA	TTC	CCG	GTT	GGG	TCA	CAG	CTC	CCG	TGT	GAG	CCC	GAA	CCG	GAT
Asn	Gln	Phe	Pro	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu	Pro	Glu	Pro	Asp
150	160	170	180	190											
GTA	ACG	GTG	ATC	ACT	TCC	ATG	CTC	ACC	GAC	CCC	TCC	CAC	ATT	ACA	GCA
Val	Thr	Val	Ile	Thr	Ser	Met	Leu	Thr	Asp	Pro	Ser	His	Ile	Thr	Ala
200	210	220	230	240											
GAG	ACG	GCT	GGG	CGT	AGG	CTG	GCC	AGA	GGG	TCT	CCC	CCT	TCC	TTG	GCC
Glu	Thr	Ala	Gly	Arg	Arg	Leu	Ala	Arg	Gly	Ser	Pro	Pro	Ser	Leu	Ala
250	260	270	280												
AGC	TCT	TCG	GCT	AGT	CAG	TTG	TCT	GCG	CCC	TCC	TTG	AAG	GCA	ACA	TGC
Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	Lys	Ala	Thr	Cys
290	300	310	320	330											
ACT	ACC	CGT	CAT	GAC	TCC	CCA	GAC	GCT	GAC	CTC	ATC	GAG	GCC	AAT	CTC
Thr	Thr	Arg	His	Asp	Ser	Pro	Asp	Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu
340	350	360	370	380											
CTG	TGG	CGG	CAG	GAG	ATG	GGA	GGG	AAC	ATC	ACC	CGC	GTG	GAG	TCA	GAG
Leu	Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu
390	400	410	420	430											
AAC	AAG	GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTC	CGA	GCG	GAG	GAG
Asn	Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	Glu
440	450	460	470	480											
GAT	GAG	AGG	GAG	ATA	TCT	GTT	GCG	GCG	GAG	ATC	CTA	CGG	AAA	TCT	AGG
Asp	Glu	Arg	Glu	Ile	Ser	Val	Ala	Ala	Glu	Ile	Leu	Arg	Lys	Ser	Arg
490	500	510	520												
AAA	TTC	CCC	CCA	GCA	TTA	CCC	ATA	TGG	GCG	CGC	CCG	GAC	TAC	AACC	
Lys	Phe	Pro	Pro	Ala	Leu	Pro	Ile	Trp	Ala	Arg	Pro	Asp	Tyr	Asn	

Fig.8

										10										20										30										40																			
GAA	TTC	TTC	ACA	GAG	TTG	GAT	GGG	GTG	CGG	CTG	CAC	AGG	TAC	GCT	CCG																																												
Glu	Phe	Phe	Thr	Glu	Leu	Asp	Gly	Val	Arg	Leu	His	Arg	Tyr	Ala	Pro																																												
										50										60										70										80										90									
GCG	TGC	AAA	CCT	CTC	CTG	CGG	GAT	GAG	GTC	ACG	TTC	CAG	GTC	GGG	CTC																																												
Ala	Cys	Lys	Pro	Leu	Leu	Arg	Asp	Glu	Val	Thr	Phe	Gln	Val	Gly	Leu																																												
										100										110										120										130										140									
AAC	CAA	TAC	CCG	GTT	GGA	TCA	CAG	CTC	CCA	TGC	GAG	CCC	GAA	CCG	GAT																																												
Asn	Gln	Tyr	Pro	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu	Pro	Glu	Pro	Asp																																												
										150										160										170										180										190									
GTG	GCG	GTG	CTC	ACT	TCC	ATG	CTC	ACC	GAC	CCC	ACC	CAC	ATT	ACA	GCA																																												
Val	Ala	Val	Leu	Thr	Ser	Met	Leu	Thr	Asp	Pro	Thr	His	Ile	Thr	Ala																																												
										200										210										220										230										240									
GAA	GCG	GCT	AGG	CGC	AGG	CTG	GCC	AGA	GGG	TCT	CCT	CCT	TCC	TTG	GCC																																												
Glu	Ala	Ala	Arg	Arg	Arg	Leu	Ala	Arg	Gly	Ser	Pro	Pro	Ser	Leu	Ala																																												
										250										260										270										280																			
AGC	TCT	TCA	GCT	AGT	CAG	TTG	TCT	GCG	CCC	TCC	TTG	AAG	GCG	ACA	TGC																																												
Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	Lys	Ala	Thr	Cys																																												
										290										300										310										320										330									
ACT	ACC	CAT	CAT	GAC	TCC	CCA	GAC	GCT	GAC	CTC	ATC	GAG	GCC	AAC	CTC																																												
Thr	Thr	His	His	Asp	Ser	Pro	Asp	Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu																																												
										340										350										360										370										380									
CTG	TGG	CGG	CAG	GAG	ATG	GGC	GGA	AAC	ATC	ACC	CGC	GTG	GAG	TCA	GAG																																												
Leu	Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu																																												
										390										400										410										420										430									
AAT	AAG	GTA	GTA	ATT	CTA	GAC	TCT	TTT	GAA	CCG	CTT	CGA	GCG	GAA	GAG																																												
Asn	Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Glu	Pro	Leu	Arg	Ala	Glu	Glu																																												
										440										450										460										470										480									
GAT	GAG	AGG	GAA	GTA	TCC	GTT	GCG	GCA	GAG	ATC	CTG	CGG	AAA	ACC	AGG																																												
Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	Arg	Lys	Thr	Arg																																												
										490										500										510										520																			
AGA	TTC	CCC	GCA	GCG	ATG	CCC	ATA	TGG	GCA	CGT	CCG	GAC	TAC	AAC	CCA																																												
Arg	Phe	Pro	Ala	Ala	Met	Pro	Ile	Trp	Ala	Arg	Pro	Asp	Tyr	Asn	Pro																																												
										530										540										550										560										570									
CCA	TTA	CTA	CAG	TCC	TGG	AAG	GAC	CCG	GAC	TAC	GTC	CCT	CCG	GTG	GTG																																												
Pro	Leu	Leu	Gln	Ser	Trp	Lys	Asp	Pro	Asp	Tyr	Val	Pro	Pro	Val	Val																																												
										580										590																																							
CAC	GGG	TGC	CCA	TTG	CCA	CCT	GC																																																				
His	Gly	Cys	Pro	Leu	Pro	Pro																																																					

Fig.9(1)

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      10      20      30      40
GAA TTC TTC ACA GAG TTG GAT GGG GTG CGG CTG CAC AGG TAC GCT CCG
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg Tyr Ala Pro

      50      60      70      80      90
GCG TGC AAA CCT CTC CTG CGG GAT GAG GTC ACG TTC CAG GTC GGG CTC
Ala Cys Lys Pro Leu Leu Arg Asp Glu Val Thr Phe Gln Val Gly Leu

      100      110      120      130      140
AAC CAA TAC CCG GTT GGA TCA CAG CTC CCA TGC GAG CCC GAA CCG GAT
Asn Gln Tyr Pro Val Gly Ser Gln Leu Pro Cys Glu Pro Glu Pro Asp

      150      160      170      180      190
GTG GCG GTG CTC ACT TCC ATG CTC ACC GAC CCC ACC CAC ATT ACA GCA
Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Thr His Ile Thr Ala

      200      210      220      230      240
GAA GCG GCT AGG CGC AGG CTG GCC AGA GGG TCT CCT CCT TCC TTG GCC
Glu Ala Ala Arg Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Leu Ala

      250      260      270      280
AGC TCT TCA GCT AGT CAG TTG TCT GCG CCC TCC TTG AAG GCG ACA TGC
Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys

      290      300      310      320      330
ACT ACC CAT CAT GAC TCC CCA GAC GCT GAC CTC ATC GAG GCC AAC CTC
Thr Thr His His Asp Ser Pro Asp Ala Asp Leu Ile Glu Ala Asn Leu

      340      350      360      370      380
CTG TGG CGG CAG GAG ATG GGC GGA AAC ATC ACC CGC GTG GAG TCA GAG
Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu

      390      400      410      420      430
AAT AAG GTA GTA ATT CTA GAC TCT TTT GAA CCG CTT CGA GCG GAA GAG
Asn Lys Val Val Ile Leu Asp Ser Phe Glu Pro Leu Arg Ala Glu Glu

      440      450      460      470      480
GAT GAG AGG GAA GTA TCC GTT GCG GCA GAG ATC CTG CGG AAA ACC AGG
Asp Glu Arg Glu Val Ser Val Ala Ala Glu Ile Leu Arg Lys Thr Arg

      490      500      510      520
AGA TTC CCC GCA GCG ATG CCC ATA TGG GCA CGT CCG GAC TAC AAC CCA
Arg Phe Pro Ala Ala Met Pro Ile Trp Ala Arg Pro Asp Tyr Asn Pro

      530      540      550      560      570
CCA TTA CTA CAG TCC TGG AAG GAC CCG GAC TAC GTC CCT CCG GTG GTG
Pro Leu Leu Gln Ser Trp Lys Asp Pro Asp Tyr Val Pro Pro Val Val

      580      590      600      610      620
CAC GGG TGC CCA TTG CCA CCT GCC AAG GCC CCT CCA GTA CCA CCT CCA
His Gly Cys Pro Leu Pro Pro Ala Lys Ala Pro Pro Val Pro Pro Pro

      630      640      650      660      670
AGG AGA AAG AGG ACG GTT GTC CTG ACA GAA TCC ACC GTG TCT TCC GCC
Arg Arg Lys Arg Thr Val Val Leu Thr Glu Ser Thr Val Ser Ser Ala

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Fig.9(2)

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      680      690      700      710      720
TTG GCG GAG CTT GCT ACA AAG ACC TTC GGC GGG TCC GGA TCA TCG GCC
Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Gly Ser Gly Ser Ser Ala

      730      740      750      760
GCC GAC AGC GGC ACA GCA AGC GGC CCT CCT GGC CAG GCC TCC GAC GAT
Ala Asp Ser Gly Thr Ala Ser Gly Pro Pro Gly Gln Ala Ser Asp Asp

      770      780      790      800      810
GGA GAT ACA GGA TCC GAC GTT GAG TCG TAC TCC TCC ATG CCC CCC CTT
Gly Asp Thr Gly Ser Asp Val Glu Ser Tyr Ser Ser Met Pro Pro Leu

      820      830      840      850      860
GAG GGA GAG CCG GGG GAC CCC GAC CTC AGC GAC GGG TCT TGG TCT ACT
Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser Trp Ser Thr

      870      880      890      900      910
GTG AGT GAG GAG GCT GGT GAG GAT GTC GTC TGC TGC TCG ATG TCC TAC
Val Ser Glu Glu Ala Gly Glu Asp Val Val Cys Cys Ser Met Ser Tyr

      920      930      940      950      960
ACA TGG ACA GGC GCC TTA ATC ACA CCA TGC ACC GCG GAG GAG AGC AAG
Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Thr Ala Glu Glu Ser Lys

      970      980      990      1000
CTG CCC ATC AAC CCG TTG AGC AAC TCT TTG CTG CGG GCA TCT GCT CGG
Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Leu Arg Ala Ser Ala Arg

      1010      1020      1030      1040      1050
GCG TAT CAT CAA CTG ATG AGC AAG AAG GAT ATA ATT CCT ACG CCC TCT
Ala Tyr His Gln Leu Met Ser Lys Lys Asp Ile Ile Pro Thr Pro Ser

      1060      1070      1080      1090      1100
CAG CCG ATG AAC AGT TGG AAT AGG TTG TTA GCG GTA ACT AAG ATT AGT
Gln Pro Met Asn Ser Trp Asn Arg Leu Leu Ala Val Thr Lys Ile Ser

      1110      1120      1130      1140      1150
ATG GTA ATT AGG AAA ATG AGT AGA TAT TTG AAG AAC TGATTAATGT
Met Val Ile Arg Lys Met Ser Arg Tyr Leu Lys Asn

      1160      1170      1180
TTGGGTCTGA GTTTATATAT CACAGTGAGA ATTC

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Fig.11

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      10      20      30      40
GAA TTC TTC ACA GAG TTG GAT GGG GTG CGG TTG CAC AGG TAC GCT CCG
Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg Tyr Ala Pro

      50      60      70      80      90
GCG TGC AAA CCT CTC CTA CGG GAT GAG GTC ACA TTT CAG GTC GGG CTC
Ala Cys Lys Pro Leu Leu Arg Asp Glu Val Thr Phe Gln Val Gly Leu

     100     110     120     130     140
AAC CAA TTC CCG GTT GGG TCA CAG CTC CCA TGT GAG CCC GAA CCG GAT
Asn Gln Phe Pro Val Gly Ser Gln Leu Pro Cys Glu Pro Glu Pro Asp

     150     160     170     180     190
GTA ACA GTG ATC ACC TCC ATG CTC ACC GAC CCC TCC CAC ATT ACA GCA
Val Thr Val Ile Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala

     200     210     220     230     240
GAG ACG GCT GGG CGT AGG CTG GCC AGA GGG TCT CCC CCT TCC TTG GCC
Glu Thr Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Leu Ala

     250     260     270     280
AGC TCT TCG GCT AGT CAG TTG TCT GCG CCT TCC TTG AAG GCG ACA TGC
Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys

     290     300     310     320     330
ACT ACC CGT CAT GAC TCC CCA GAC GCT GAC CTC ATC GAG GCC AAT CTC
Thr Thr Arg His Asp Ser Pro Asp Ala Asp Leu Ile Glu Ala Asn Leu

     340     350     360     370     380
CTG TGG CGG CAG GAG ATG GGA GGG AAC ATC ACC CGC GTG GAG TCA GAG
Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu

     390     400     416     420     430
AAC AAG GTA GTA ATC CTA GAC TCT TTT GAC CCG CTC CGA GCG GAG GAG
Asn Lys Val Val Ile Leu Asp Ser Phe Asp Pro Leu Arg Ala Glu Glu

     440     450     460     470     480
GAT GAG AGG GAG ATA TCT GTT GCG GCG GAG ATC CTA CGG AAA TCT AGG
Asp Glu Arg Glu Ile Ser Val Ala Ala Glu Ile Leu Arg Lys Ser Arg

     490     500     510     520
AAA TTC CCC CCA GCA TTA CCC ATA TGG GCG CGC CCG GAC TAC AAC CCA
Lys Phe Pro Pro Ala Leu Pro Ile Trp Ala Arg Pro Asp Tyr Asn Pro

     530     540     550
CCA CTG CTA GAG TCT TGG CCA GCT G
Pro Leu Leu Glu Ser Trp Pro Ala

```

Fig.12(1)

	10		20		30		40								
CG	GCT	TTC	GTG	GGC	GCC	GGC	ATA	GCC	GGC	GCG	GCT	GTT	GGC	AGC	ATA
	Ala	Phe	Val	Gly	Ala	Gly	Ile	Ala	Gly	Ala	Ala	Val	Gly	Ser	Ile
50		60		70		80		90							
GGC	CTT	GGG	AAG	GTG	CTT	GTG	GAC	ATC	CTG	GCG	GGT	TAT	GGA	GCA	GGG
Gly	Leu	Gly	Lys	Val	Leu	Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	Gly
100		110		120		130		140							
GTG	GCA	GGC	GCA	CTC	GTG	GTC	TTT	AAG	GTT	ATG	AGT	GGC	GAC	ATG	CCC
Val	Ala	Gly	Ala	Leu	Val	Val	Phe	Lys	Val	Met	Ser	Gly	Asp	Met	Pro
150		160		170		180		190							
TCC	ACC	GAG	GAC	CTG	GTC	AAC	TTA	CTC	CCT	GCC	ATC	CTT	TCC	CCT	GGC
Ser	Thr	Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	Gly
200		210		220		230									
GCC	CTG	GTC	GTC	GGG	GTC	GTG	TGC	GCA	CAG	ATA	CTG	CGT	CGA	CAT	GTC
Ala	Leu	Val	Val	Gly	Val	Val	Cys	Ala	Gln	Ile	Leu	Arg	Arg	His	Val
240		250		260		270		280							
GGC	CCA	GGG	GAG	GGA	GCT	GTG	CAG	TGG	ATG	AAC	CGG	CTG	ATA	GCG	TTC
Gly	Pro	Gly	Glu	Gly	Ala	Val	Gln	Trp	Met	Asn	Arg	Leu	Ile	Ala	Phe
290		300		310		320		320							
GCT	TCG	CGG	GGT	AAC	CAC	GTC	TCC	CCC	ACG	CAT	TAT	GTG	CCT	GAA	AGC
Ala	Ser	Arg	Gly	Asn	His	Val	Ser	Pro	Thr	His	Tyr	Val	Pro	Glu	Ser
340		350		360		370		380							
GAC	GCT	GCG	AGT	CGT	GTC	ACC	CAG	ATC	CTC	TCC	AGC	CTT	ACC	ATC	ACT
Asp	Ala	Ala	Ser	Arg	Val	Thr	Gln	Ile	Leu	Ser	Ser	Leu	Thr	Ile	Thr
390		400		410		420		430							
CAG	CTG	TTG	AAG	AGG	CTC	CAC	CAG	TGG	ATT	AAT	GAG	GAC	TGC	TCC	ACG
Gln	Leu	Leu	Lys	Arg	Leu	His	Gln	Trp	Ile	Asn	Glu	Asp	Cys	Ser	Thr
440		450		460		470									
CCA	TGC	TCC	GGC	ACG	TGG	CTC	AGG	GAT	GTT	TGG	GAC	TGG	ATA	TGC	ACG
Pro	Cys	Ser	Gly	Thr	Trp	Leu	Arg	Asp	Val	Trp	Asp	Trp	Ile	Cys	Thr
480		490		500		510		520							
GTG	TTG	GCT	GAC	TTC	AAG	ACC	TGG	CTC	CAG	TCC	AAG	CTC	CTG	CCG	CGG
Val	Leu	Ala	Asp	Phe	Lys	Thr	Trp	Leu	Gln	Ser	Lys	Leu	Leu	Pro	Arg
530		540		550		560		570							
TTA	CCG	GGG	GTC	CCT	TTC	CTC	TCA	TGT	CAG	CGT	GGG	TAC	AAG	GGA	GTT
Leu	Pro	Gly	Val	Pro	Phe	Leu	Ser	Cys	Gln	Arg	Gly	Tyr	Lys	Gly	Val
580		590		600		610		620							
TGG	CGG	GGA	GAT	GGC	ATC	ATG	CAC	ACC	ACC	TGC	CCA	TGC	GGA	GCC	CAA
Trp	Arg	Gly	Asp	Gly	Ile	Met	His	Thr	Thr	Cys	Pro	Cys	Gly	Ala	Gln
630		640		650		660		670							
ATC	ACC	GGA	CAT	GTC	AAA	AAC	GGG	TCC	ATG	AGG	ATC	GCC	GGG	CCT	AAA
Ile	Thr	Gly	His	Val	Lys	Asn	Gly	Ser	Met	Arg	Ile	Ala	Gly	Pro	Lys

Fig.12(2)

			680				690				700				710				
ACC	TGC	AGC	AAC	ACG	TGG	CAC	GGA	ACG	TTC	CCC	ATT	AAC	GCA	TAC	ACC				
Thr	Cys	Ser	Asn	Thr	Trp	His	Gly	Thr	Phe	Pro	Ile	Asn	Ala	Tyr	Thr				
720				730				740				750				760			
ACA	GGC	CCC	TGC	ACA	CCC	TCT	CCG	GCG	CCA	AAC	TAC	TCC	AGG	GCG	TTG				
Thr	Gly	Pro	Cys	Thr	Pro	Ser	Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala	Leu				
	770				780				790				800				810		
TGG	CGG	GTG	GCT	GCG	GAG	GAG	TAC	GTG	GAG	GTC	ACG	CGG	GTG	GGG	GAT				
Trp	Arg	Val	Ala	Ala	Glu	Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly	Asp				
		820				830				840			850				860		
TTC	CAC	TAC	GTG	ACG	GGC	ATG	ACC	ACT	GAC	AAT	GTA	AAA	TGC	CCA	TGC				
Phe	His	Tyr	Val	Thr	Gly	Met	Thr	Thr	Asp	Asn	Val	Lys	Cys	Pro	Cys				
			870				880												
CAG	GTT	CCG	GCC	CCC	GAA	TTC													
Gln	Val	Pro	Ala	Pro	Glu	Phe													

Fig.13

	10		20		30		40								
GAA	TTC	TTC	ACA	GAG	TTG	GAC	GGG	GTG	CGG	CTG	CAC	AGG	TAC	GCT	CCG
Glu	Phe	Phe	Thr	Glu	Leu	Asp	Gly	Val	Arg	Leu	His	Arg	Tyr	Ala	Pro
50		60		70		80		90							
GCG	TGC	AGA	CCT	CTC	CTG	CGG	GAT	GAG	GTC	ACA	TTC	CAG	GTC	GGG	CTC
Ala	Cys	Arg	Pro	Leu	Leu	Arg	Asp	Glu	Val	Thr	Phe	Gln	Val	Gly	Leu
100		110		120		130		140							
AAC	CAA	TAC	CCG	GTT	GGG	TCA	CAG	CTC	CCA	TGT	GAG	CCC	GAA	CCG	GAT
Asn	Gln	Tyr	Pro	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu	Pro	Glu	Pro	Asp
150		160		170		180		190							
GTA	ACA	GTG	GTC	ACT	TCC	ATG	CTC	ACC	GAC	CCC	TCC	CAC	ATT	ACA	GCG
Val	Thr	Val	Val	Thr	Ser	Met	Leu	Thr	Asp	Pro	Ser	His	Ile	Thr	Ala
200		210		220		230		240							
GAA	ACT	GCC	AGG	CGT	AGG	TTG	GCC	AGG	GGG	AGT	CCC	CCT	TCC	TTG	GCC
Glu	Thr	Ala	Arg	Arg	Arg	Leu	Ala	Arg	Gly	Ser	Pro	Pro	Ser	Leu	Ala
250		260		270		280									
AGC	TCT	TCA	GCT	AGT	CAG	TTG	TCT	GCA	CCT	TCC	TTG	AAG	GCG	ACA	TGT
Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	Lys	Ala	Thr	Cys
290		300		310		320		330							
ACT	ACC	CAT	CAT	GAC	TCT	CCA	GAC	GCT	GAT	CTC	ATC	GAG	GCC	AAC	CTT
Thr	Thr	His	His	Asp	Ser	Pro	Asp	Ala	Asp	Leu	Ile	Glu	Ala	Asn	Leu
340		350		360		370		380							
CTA	TGG	CGG	CAG	GAG	ATG	GGC	GGG	AAC	ATC	ACC	CGT	GTG	GAG	TCA	GAG
Leu	Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu
390		400		410		420		430							
AAT	AAG	GTA	GTA	ATC	CTA	GAC	TCT	TTT	GAC	CCG	CTT	CGA	GCG	GAG	GAG
Asn	Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Arg	Ala	Glu	Glu
440		450		460		470		480							
GAT	GAG	AGG	GAA	GTA	TCC	GTT	GCG	GCG	GAG	ATC	CTG	CGG	AGA	ACC	AGG
Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	Arg	Arg	Thr	Arg
490		500		510		520									
AGA	TTC	CCC	CCG	GCG	ATA	CCT	GTA	TGG	GCG	CGC	CCG	GAC	CAG	CT	
Arg	Phe	Pro	Pro	Ala	Ile	Pro	Val	Trp	Ala	Arg	Pro	Asp	Gln		

Fig.14

			10				20				30				40			
GAA	TTC	AGC	AAA	GTT	TCC	AGA	TAC	AAG	ATT	AAT	GGA	CAC	AAA	TCA	GTA			
Glu	Phe	Ser	Lys	Val	Ser	Arg	Tyr	Lys	Ile	Asn	Gly	His	Lys	Ser	Val			
			50				60				70				80			90
GCT	CTT	CCA	TAC	ATC	AAC	AGC	TAC	CAA	GCA	GAG	AAT	CAC	ATC	AAG	AAC			
Ala	Leu	Pro	Tyr	Ile	Asn	Ser	Tyr	Gln	Ala	Glu	Asn	His	Ile	Lys	Asn			
			100				110				120				130			140
TCA	ACC	CCT	TTT	ACA	ATA	GCT	GCG	ACA	AAC	AAC	AAC	AAC	AAA	AAA	ACA			
Ser	Thr	Pro	Phe	Thr	Ile	Ala	Ala	Thr	Asn	Asn	Asn	Asn	Lys	Lys	Thr			
			150				160				170							
AAA	CTT	AGG	AAT	ATA	CCT	AGC	AAA	GAA	TTC									
Lys	Leu	Arg	Asn	Ile	Pro	Ser	Lys	Glu	Phe									

Fig.15

			10			20			30			40			
GAA	TTC	CCT	AGC	CTG	GGC	AAC	AGA	GTG	AGA	GTC	CGT	CTC	AAA	AAA	AAA
Glu	Phe	Pro	Ser	Leu	Gly	Asn	Arg	Val	Arg	Val	Arg	Leu	Lys	Lys	Lys
50			60			70			80			90			
AAA	ACA	ACA	ACA	AAA	AAA	ACA	AAC	CCA	CAA	AAC	TGC	AGC	CAC	CTA	TGT
Lys	Thr	Thr	Thr	Lys	Lys	Thr	Asn	Pro	Gln	Asn	Cys	Ser	His	Leu	Cys
	100			110			120			130					
CCC	TAC	CTC	CCC	AGC	CTC	CAG	GGC	CCC	TTC	CGG	AAT	TCC			
Pro	Tyr	Leu	Pro	Ser	Leu	Gln	Gly	Pro	Phe	Arg	Asn	Ser			

Fig.16

	10		20		30		40								
GAA	TTC	GCG	GGA	ACC	CGG	GAG	GCG	GAC	GTT	GCA	GTG	AGC	CGA	GAT	CGC
Glu	Phe	Ala	Gly	Thr	Arg	Glu	Ala	Asp	Val	Ala	Val	Ser	Arg	Asp	Arg
50		60		70		80		90							
GCC	ACT	GCA	CTC	CAG	CCT	GGG	CGA	CAG	AGC	AAG	ACT	CTG	TCT	CAA	AAA
Ala	Thr	Ala	Leu	Gln	Pro	Gly	Arg	Gln	Ser	Lys	Thr	Leu	Ser	Gln	Lys
100		110		120		130									
AAA	AAA	AAC	AAA	AAC	AAA	AAG	AAG	GAC	TGG	GAG	GGT	CGG	CAG		
Lys	Lys	Asn	Lys	Asn	Lys	Lys	Lys	Asp	Trp	Glu	Gly	Arg	Gln		
140		150		160		170		180							
TAATCGAGGA	CCACCTGGCA	GTGACAGAGG	GTGACCCAGG	GCTGGGAGGA											
190		200		210		220		230							
TACCCCAGGG	GAGACCCAG	GCTCTGAAAA	GTGCCTTGCC	ATTCAATCTA											
240		250		260		270		280							
CTTCAGTAAT	AGCATGTGTC	ATGGGATAGA	TAATAAAATC	CGGAGGGGAA											
290		300													
AAAATGCTCG	CGGAATTC														

Fig.17

	10	20	30	40	
GAA TTC AGC ACA GTT TCC AGA TAC AAG ATT AAT GGA CAC AAA TCA GTA					
Glu Phe Ser Thr Val Ser Arg Tyr Lys Ile Asn Gly His Lys Ser Val					
50	60	70	80	90	
GCT CTT CCA TAC ATC AAC AGC TAC CAA GCA GAG AAT CAC ATC AAG AAC					
Ala Leu Pro Tyr Ile Asn Ser Tyr Gln Ala Glu Asn His Ile Lys Asn					
100	110	120	130	140	
TCA ACC CCT TTT ACA ATA GCT GCG ACA AAC AAC AAC AAC AAA AAA ACA					
Ser Thr Pro Phe Thr Ile Ala Ala Thr Asn Asn Asn Asn Lys Lys Thr					
150	160	170			
AAA CTT AGG AAT ATA CCT AGC AAA GAA TTC					
Lys Leu Arg Asn Ile Pro Ser Lys Glu Phe					

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Fig.19

10 20 30 40
 GAA TTC TTC ACG GAA TTG GAT GGG GTG CCG CTA CAC AGG TAC GCT CCG
 Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg Tyr Ala Pro
 50 60 70 80 90
 GCG TGC AAG CCT CTC CTA CGG GAT GAG GTC ACA TTC CAG GTC GGG CTC
 Ala Cys Lys Pro Leu Leu Arg Asp Glu Val Thr Phe Gln Val Gly Leu
 100 110 120 130 140
 AAC CAA TTC CCG GTT GGG TCA CAG CTC CCA TGT GAA CCC GAA CCG GAT
 Asn Gln Phe Pro Val Gly Ser Gln Leu Pro Cys Glu Pro Glu Pro Asp
 150 160 170 180 190
 GTA ATG GTG GTC ACC TCT ATG CTC ACC GAC CCC TCC CAT ATT ACA GCA
 Val Met Val Val Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala
 200 210 220 230 240
 GAG ACG GCT AAG CGT AGG CTG GCC AGA GGG TCT CCC CCT TCT TTG GCC
 Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Leu Ala
 250 260 270 280
 AGC TCT TCA GCT AGT CAG TTG TCT GCG CCC TCC TTG AAG GCG ACA TGC
 Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys
 290 300 310 320 330
 ACC ACC CGT CAT GAC TCC CCG GAC GCT GAC CTC ATA GAG GCC AAC CTC
 Thr Thr Arg His Asp Ser Pro Asp Ala Asp Leu Ile Glu Ala Asn Leu
 340 350 360 370 380
 CTG TGG CGG CAG GAG ATG GGC GGG AAC ATC ACC CGT GTG GAG TCA GAG
 Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val Glu Ser Glu
 390 400 410 420 430
 AAT AAG GTA GTG ATT TTG GAC TCT TTT GAA CCG CTT CGG GTG GAG GAG
 Asn Lys Val Val Ile Leu Asp Ser Phe Glu Pro Leu Arg Val Glu Glu
 440 450 460 470 480
 GAT GAG AGG GAA GTA TCC GTA GCG GCG GAT TTC AGT GAC TTG AAT GCA
 Asp Glu Arg Glu Val Ser Val Ala Ala Asp Phe Ser Asp Leu Asn Ala
 490 500 510 520 530
 GAA TGAATCCCGT GGCTCACTTC CTAGACTATT TGCCAAAGAA GATGTTGCCC
 Glu
 540 550 560 570 580
 TGGCCATGAT CAAGATGACA CAAACGGTGG CCTTTTGCAG GGAGAACCGC
 590 600 610 620 630
 CGTGGAGGCC TGTGTCTGTG GCACTGGTAG CTTCTCTCTG CAGGCAAAGA
 640 650 660
 CCCCATGGCT TAGTTCTTCA TCAGAGTGAG AATTC

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Fig.21

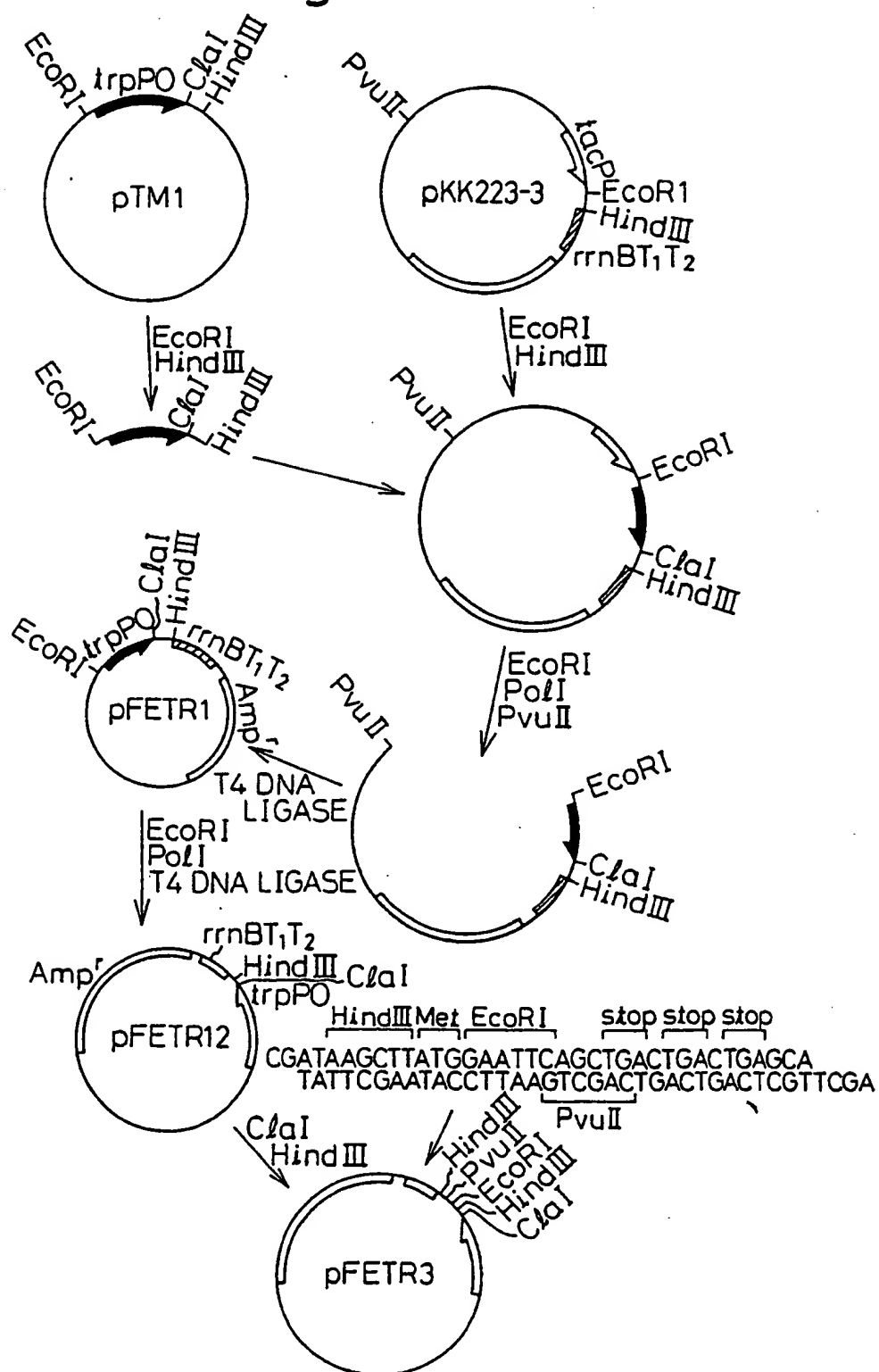


Fig.22

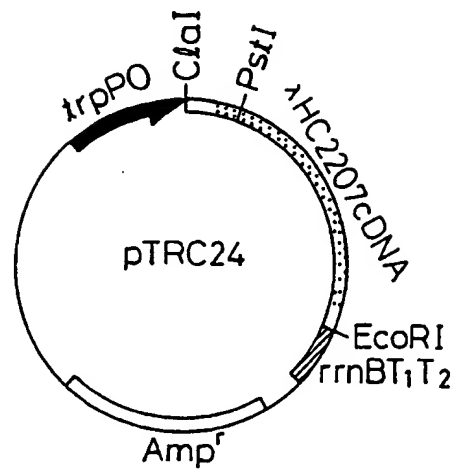
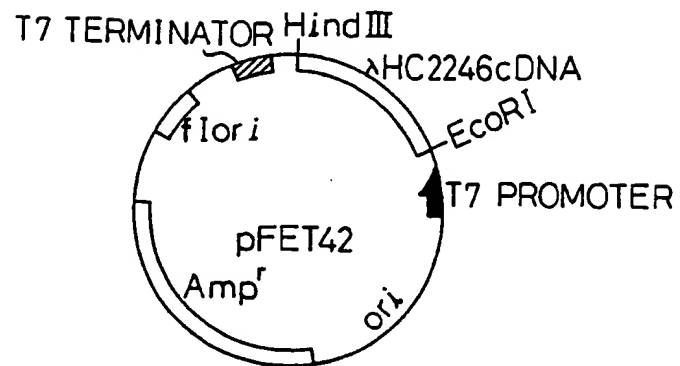


Fig.23





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European Patent Office
Office européen des brevets



Publication number: **0 416 725 A3**

(12)

EUROPEAN PATENT APPLICATION

(21) Application number: 90307566.1

(51) Int. Cl.⁵: **C12N 15/51, C07K 15/00,
//A61K39/29, G01N33/576**

(22) Date of filing: 11.07.90

(30) Priority: 14.07.89 JP 182073/89
19.07.89 JP 184739/89
22.07.89 JP 189874/89
27.07.89 JP 192721/89
29.07.89 JP 195413/89
03.08.89 JP 200217/89
10.08.89 JP 205722/89
21.09.89 JP 243304/89
22.09.89 JP 245268/89
19.10.89 JP 270398/89

(43) Date of publication of application:
13.03.91 Bulletin 91/11

(64) Designated Contracting States:
AT BE CH DE DK ES FR GB GR IT LI NL SE

(96) Date of deferred publication of the search report:
20.03.91 Bulletin 91/12

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(54) **Blood-borne non-A, non-B hepatitis specific protein, DNA encoding it, and process for its production.**

(57) A DNA coding for a blood-borne non-A, non-B hepatitis specific antigenic protein and corresponding to an RNA directly isolated from a human blood or liver tissue is disclosed. This antigenic protein can be produced by using the DNA, and the antigenic protein binds to an antibody in the serum of the patient with the non-A, non-B hepatitis. Therefore, the antigenic protein is useful for the diagnostic measurement of an antibody against the non-A, non-B hepatitis specific antigen.

EP 0 416 725 A3



European
Patent Office

EUROPEAN SEARCH REPORT

Application Number

EP 20 30 7566

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.5)
X	EP-A-0 318 216 (CHIRON CORP.) * The whole document, especially figures 28,32 * - - -	1-12	C 12 N 15/51 C 07 K 15/00 // A 61 K 39/29 G 01 N 33/576
E	EP-A-0 388 232 (CHIRON CORP.) * Claims * - - - - -	1-12	
			TECHNICAL FIELDS SEARCHED (Int. Cl.5)
			C 07 K C 12 N A 61 K
The present search report has been drawn up for all claims			
Place of search The Hague		Date of completion of search 18 December 90	Examiner SKELLY J.M.
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